

GenCore version 5.1.7  
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## OM protein - protein search, using sw model

Run on: April 3, 2006, 08:02:30 ; Search time 81 Seconds  
(without alignments)  
86.791 Million cell updates/sec

Title: US-09-647-457F-3  
Perfect score: 90  
Sequence: 1 LVVGLCTCQIKTGAPAC 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A\_Geneseq\_21:.\*  
1: geneseqp1980e:.\*  
2: geneseqp1980e:.\*  
3: geneseqp2000e:.\*  
4: geneseqp2000e:.\*  
5: geneseqp2002e:.\*  
6: geneseqp2003as:.\*  
7: geneseqp2003bs:.\*  
8: geneseqp2004e:.\*  
9: geneseqp2005e:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	100.0	16	2	AAV43191 Schizophr
2	78	86.7	16	2	AAV43204 Schizophr
3	78	86.7	17	2	AAV43198 Schizophr
4	78	86.7	17	2	AAV43197 Schizophr
5	74	82.2	458	6	AAV43197 Carbohydr
6	74	82.2	458	8	ADQ30526 Pancreas
7	74	82.2	458	7	ADQ30526 Pancreas
8	74	82.2	458	7	ADQ30526 Pancreas
9	65	72.2	16	2	AAV43202 Schizophr
10	65	72.2	17	2	AAV43196 Schizophr
11	65	72.2	18	2	AAV43195 Schizophr
12	65	72.2	19	2	AAV43194 Schizophr
13	65	72.2	20	2	AAV43193 Schizophr
14	65	72.2	28	2	AAV43192 Schizophr
15	65	72.2	50	8	ADU78952 Human pro
16	65	72.2	156	8	ADU78952 Human pro
17	65	72.2	269	6	ADU78952 Human pro
18	65	72.2	269	6	ADU78952 Human pro
19	65	72.2	272	6	ABU04378 Human exp
20	65	72.2	272	6	ABU04378 Human exp
21	65	72.2	336	6	ABU04376 Human exp
22	65	72.2	420	6	AAE38225 Human enz
23	65	72.2	429	6	ABU03958 Human exp
24	65	72.2	433	2	AAW14001 Enolase p

25	65	72.2	433	2	AAW54357 Alpha Eno
26	65	72.2	433	6	ABU03944 Human exp
27	65	72.2	433	6	ABU03942 Human exp
28	65	72.2	433	8	ADQ30574 Pancreas
29	65	72.2	434	5	ABBS7379 Rat mucoc
30	65	72.2	434	5	ABPE5147 Hypoxia-r
31	65	72.2	434	5	ABPE5155 Hypoxia-r
32	65	72.2	434	5	AAW48922 Human eno
33	65	72.2	434	6	ABPE4211 Angiogene
34	65	72.2	434	6	ABR77446 Breast ca
35	65	72.2	434	6	ABR59704 Human eno
36	65	72.2	434	6	ABU03929 Human exp
37	65	72.2	434	6	ABU03943 Human exp
38	65	72.2	434	6	ABU03934 Human exp
39	65	72.2	434	6	ABU03936 Human exp
40	65	72.2	434	6	ABU03935 Human exp
41	65	72.2	434	6	ABU03932 Human exp
42	65	72.2	434	6	ABU03930 Human exp
43	65	72.2	434	6	ABU03931 Human exp
44	65	72.2	434	6	ABU03937 Human exp
45	65	72.2	434	6	ABU03933 Human exp
46	65	72.2	434	6	ABU04797 Human alp
47	65	72.2	434	6	ADB85166 Rat enola
48	65	72.2	434	7	ADCS2079 Human adi
49	65	72.2	434	7	ADQ27706 Human pro
50	65	72.2	434	7	ADQ38355 Human pro
51	65	72.2	434	7	ADQ76365 Novel hum
52	65	72.2	434	7	ADQ95644 Human BEC
53	65	72.2	434	7	ADPE5133 Human eno
54	65	72.2	434	8	ADN04765 Antipsoxi
55	65	72.2	434	8	ADP12542 Protein e
56	65	72.2	434	8	ADQ19151 Human PRO
57	65	72.2	434	8	ADQ18898 Human sof
58	65	72.2	434	8	ADQ19129 Human sof
59	65	72.2	434	8	ADQ67648 Human eno
60	65	72.2	434	8	ADQ67650 Human eno
61	65	72.2	434	8	ADQ67646 Human eno
62	65	72.2	434	8	ABW80012 Tumour-as
63	65	72.2	434	8	ABW81339 Tumour-as
64	65	72.2	434	8	ADP54197 Human PRO
65	65	72.2	434	8	ADP23174 PRO polyP
66	65	72.2	434	9	ADW07263 Human hep
67	65	72.2	434	9	ADY19632 PRO polyP
68	65	72.2	434	9	ADY75135 Brain tum
69	65	72.2	434	9	ADZ70552 Human pro
70	65	72.2	434	9	ABE16877 Rat neuro
71	65	72.2	434	9	ABE16883 Human neu
72	65	72.2	434	9	ABE16875 Rat neuro
73	65	72.2	434	9	ABE16884 Rat neuro
74	65	72.2	434	5	ABE16885 Human neu
75	65	72.2	438	5	ABP43623 Enolase 1
76	61	67.8	16	2	AAV43200 Schizophr
77	59	65.6	432	7	ADD26937- Human adi
78	59	65.6	434	9	AEA51198 Chicken g
79	58	65.6	434	9	ABE16886 Chicken n
80	58	64.4	15	2	AAV43203 Schizophr
81	56	62.2	396	9	ADY71461 Trichine1
82	56	62.2	434	8	ADN22854 Bacteri1
83	56	62.2	437	9	ADY71463 Trichine1
84	55	61.1	433	4	ABB67951 Drosoph11
85	51	56.7	66	5	ABP34165 Human hyd
86	51	56.7	68	3	AAQ20166 Arabidops
87	51	56.7	77	3	AAQ20165 Arabidops
88	51	56.7	78	3	AAQ20164 Arabidops
89	51	56.7	211	8	ADY95179 Plant ful
90	51	56.7	245	8	ADY7369 Plant ful
91	51	56.7	313	7	ABW89093 Rice abio
92	51	56.7	340	7	ADM67652 D. salina
93	51	56.7	352	3	AAQ37553 Arabidops
94	51	56.7	443	7	ABW73839 DNA clone
95	51	56.7	444	3	AAQ37552 Arabidops
96	51	56.7	444	9	AEA60820 Arabidops
97	51	56.7	469	3	AAQ37551 Arabidops

98	50	55.6	152	8	ADX80391	Plant full
99	50	55.6	226	8	ADX93896	Plant full
100	50	55.6	284	8	ADX74478	Plant full

## ALIGNMENTS

## RESULT 1

AAV43191  
ID AAV43191 standard; peptide; 16 AA.

AC AAV43191;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #1.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;  
platelet-associated antibody; diagnosis.

OS Synthetic.

PN MO9951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL000190.

PR 02-APR-1998; 98IL-00123925.

PA (YEDA ) YEDA RES & DEV CO LTD.

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

PT New peptides useful for diagnosis of schizophrenia.

PS Claim 2; Page 21; 37pp; English.

CC This sequence is a peptide of the invention, which binds antibodies found  
CC in elevated levels in body fluids of schizophrenic patients. The peptide  
CC is useful in an assay for the diagnosis of schizophrenia, by binding the  
CC peptide to a platelet-containing fraction of blood, or a fraction  
CC containing platelet-associated antibodies (PAA) shed from the platelets,  
CC or preferably whole blood. The new peptides are able to differentiate  
CC between plasma samples from schizophrenic and non-schizophrenic patients,  
CC and can do so without having to first isolate the platelet-associated  
CC antibodies (PAA) fraction

SQ Sequence 16 AA;

Query Match 100.0%; Score 90; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.1e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGPAAC 16  
Db 1 LVVGLCTGQIKTGPAAC 16

## RESULT 2

AAV43204  
ID AAV43204 standard; peptide; 16 AA.

AC AAV43204;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #14.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;  
Schizophrenic derived antibody; binding epitope; schizophrenia;

KW platelet-associated antibody; diagnosis.

OS Synthetic.

PN MO9951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL000190.

PR 02-APR-1998; 98IL-00123925.

PA (YEDA ) YEDA RES & DEV CO LTD.

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

PT New peptides useful for diagnosis of schizophrenia.

PS Claim 4; Page 21; 37pp; English.

CC This sequence is a peptide of the invention, which binds antibodies found  
CC in elevated levels in body fluids of schizophrenic patients. The peptide  
CC is useful in an assay for the diagnosis of schizophrenia, by binding the  
CC peptide to a platelet-containing fraction of blood, or a fraction  
CC containing platelet-associated antibodies (PAA) shed from the platelets,  
CC or preferably whole blood. The new peptides are able to differentiate  
CC between plasma samples from schizophrenic and non-schizophrenic patients,  
CC and can do so without having to first isolate the platelet-associated  
CC antibodies (PAA) fraction

SQ Sequence 16 AA;

Query Match 86.7%; Score 78; DB 2; Length 16;  
Best Local Similarity 93.8%; Pred. No. 0.00089;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGPAAC 16  
Db 1 LVVGLCTGQIKTGPAAC 16

## RESULT 3

AAV43198  
ID AAV43198 standard; peptide; 17 AA.

AC AAV43198;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #8.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;  
platelet-associated antibody; diagnosis.

OS Synthetic.

PN MO9951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL000190.

PR 02-APR-1998; 98IL-00123925.

PA (YEDA ) YEDA RES & DEV CO LTD.

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

PT New peptides useful for diagnosis of schizophrenia.



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FT      /note= "Identified by PROFILESCAN"
FT      331..366
FT      /label= Enolase protein
FT      /note= "Identified by BLIMPS_BLOCKS"
FT      335..346
FT      /label= Enolase signature
FT      /note= "Identified by BLIMPS_PRINTS"
FT      361..375
FT      /label= Enolase signature
FT      /note= "Identified by BLIMPS_PRINTS"
FT      392..409
FT      /label= Enolase signature
FT      /note= "Identified by BLIMPS_PRINTS"
FT      403..441
FT      /label= Enolase protein
FT      /note= "Identified by BLIMPS_BLOCKS"
FT      408..456
FT      /label= Enolase lyase glycolysis
FT      /note= "Identified by BLAST_PRODOW"

XX      WO200297060-A2.
XX      PD
XX      05-DEC-2002.
XX      PF
XX      22-MAY-2002; 2002WO-US018354.
XX      PR
XX      25-MAY-2001; 2001US-0293768P.
XX      PR      01-AUG-2001; 2001US-0309548P.
XX      PR      23-AUG-2001; 2001US-0314400P.
XX      PR      19-OCT-2001; 2001US-0343706P.
XX      PR      07-DEC-2001; 2001US-0337999P.
XX      PA
XX      (INCY-) INCYTE GENOMICS INC.
XX      PI
XX      Swarnakar A, Gorvad AE, Hafalia AJA, Duggan BM, Emerling BM;
XX      Ison CH, Nguyen DB, Lee EA, Yue H, Forgythe TJ, Li JX;
XX      Thangavelu K, Walla NK, Burford N, Mason PM, Lal PG, Lee S;
XX      Becha SD, Tang YT;
XX      WPI; 2003-140462/13.
XX      DR      N-PSDB; ABA00836.
XX      PT
XX      Novel human carbohydrate associated polypeptide, useful in diagnosis,
XX      treatment and prevention of carbohydrate metabolism, cell proliferative,
XX      autoimmune/inflammatory, reproductive, and neurological disorders.
XX      PS
XX      Claim 1; Page 129-30; 141pp; English.
XX      CC
XX      The sequences given in AAG79779-88 represent human carbohydrate
XX      associated polypeptides (CHOP). The CHOP polypeptides and the nucleotide
XX      sequences encoding them, are useful for diagnosing, treating and
XX      preventing cancer, carbohydrate metabolic disorders (e.g. diabetes,
XX      anaemia, hypoglycaemia, obesity, glycogen storage disease, neurological
XX      dysfunction), cell proliferative disorders (e.g. actinic keratosis,
XX      arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, psoriasis),
XX      autoimmune/inflammatory disorders (such as acquired immunodeficiency,
XX      syndrome (AIDS), Addison's disease, allergies, asthma, contact
XX      dermatitis, bronchitis, gout, Hashimoto's thyroiditis), viral, bacterial,
XX      fungal, parasitic, protozoal and helminthic infections, reproductive
XX      disorders (e.g. endometriosis, polycystic ovary syndrome, ovarian
XX      hyperstimulation syndrome), genetic disorders (e.g. Down syndrome, cystic
XX      fibrosis, sickle cell anaemia, thalassemia), cardiac disorders (e.g.
XX      myocarditis, cardiomyopathy), neurological disorders (e.g.
XX      Alzheimer's disease, dementia, depression, epilepsy, Tourette's
XX      disorder, Schizophrenia), and developmental disorders of central nervous
XX      system (e.g. cerebral palsy), mental disorders (e.g. mood, anxiety). CHOP
XX      proteins are useful in a number of drug screening techniques, and to
XX      analyse the proteome of a tissue or cell type. CHOP cDNA is useful for
XX      creating "knockin" humanized animals or transgenic animals to model human
XX      diseases, in somatic or germline gene therapy, to generate a transcript
XX      image of a tissue or cell type, for detecting differences in the
XX      chromosomal location due to translocation, inversion, etc., among normal,
XX      carrier or affected individuals, and as hybridization probes for mapping

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CC      naturally occurring genomic sequences
XX      SQ      Sequence 458 AA;
XX      Query Match      82.2%; Score 74; DB 6; Length 458;
XX      Best Local Similarity 87.5%; Pred. No. 0.056;
XX      Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX      QY      1 LVVGLCTGQIKTGSPAC 16
XX      Db      407 LVVGLCTGQIKTGSPAC 422
XX      RESULT 6
XX      ID      ADQ30526
XX      ADQ30526 standard; protein; 458 AA.
XX      AC      ADQ30526;
XX      DT      23-SEP-2004 (first entry)
XX      DE      Pancreas cancer marker - alpha enolase.
XX      KM      Cytostatic; diagnosis; pancreatic cancer; antibody; antisense construct;
XX      KM      differential expression.
XX      OS      Homo sapiens.
XX      PN      WO2004055519-A2.
XX      PD      01-JUL-2004.
XX      PF      11-DEC-2003; 2003WO-EP014057.
XX      PR      17-DEC-2002; 2002EP-00028058.
XX      PR      05-NOV-2003; 2003EP-00025237.
XX      PA      (HOPF ) HOPFMANN LA ROCHE & CO AG F.
XX      (SINO-) SINOGENOMAX CO LTD CHINESE NAT HUMAN GEN.
XX      PI      Chen J, Hu L, Liu TH, Lu ZH, Shen Y;
XX      WPI; 2004-488121/46.
XX      PT      New specific markers comprises at least one polypeptide up-regulated in
XX      pancreatic cancer, useful for diagnosing pancreatic cancer.
XX      PS      Claim 1; SEQ ID NO 13; 381pp; English.
XX      CC
XX      The invention relates to a marker (I) for diagnosis of pancreatic cancer
XX      comprising at least one polypeptide selected from 55 proteins up-
XX      regulated in pancreatic cancer (Table 2 and Table 3, given in the
XX      specification) or from 68 proteins with higher levels in pancreatic
XX      cancer compared to normal tissue (Table 6, given in the specification).
XX      (I) is a polypeptide for use as a marker or as a component of a marker
XX      for diagnosis of pancreatic cancer and/or the susceptibility to
XX      pancreatic cancer. A compound (antibody, an antibody-derivative, an
XX      antibody fragment, a peptide, or an antisense construct) identified by
XX      screening methods using (I) is useful for treatment or prevention of
XX      pancreatic cancer. It is also useful for the preparation of a diagnostic
XX      composition for diagnosing pancreatic cancer or a predisposition for
XX      pancreatic cancer. The current polypeptides were found to be
XX      differentially expressed in pancreatic tissue obtained from individuals
XX      suffering from pancreatic cancer as compared to healthy pancreatic
XX      tissue. They have been identified as suitable as markers of pancreatic
XX      cancer for early diagnosis of the disease. This sequence corresponds to a
XX      protein marker of the invention.
XX      SQ      Sequence 458 AA;
XX      Query Match      82.2%; Score 74; DB 8; Length 458;
XX      Best Local Similarity 87.5%; Pred. No. 0.056;
XX      Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Oy 1 LVVGLCTGQIKTGPAAC 16  
 |||||  
 Db 407 LVVGLCTGQIKTGPTC 422

RESULT 7  
 ADM08691  
 ID ADM08691 standard; protein; 458 AA.  
 AC ADM08691;  
 DT 24-MAR-2005 (first entry)

DE Human protein which is down-regulated in HCV-infected tissue - SEQ ID 28.  
 XX  
 KM gene targeting; hepatitis C virus infection; protein deactivation;  
 KM protein activation.

OS Homo sapiens.

XX EP1493750-A2.

XX 05-JAN-2005.

XX 28-JUN-2004; 2004EP-00015098.

XX 30-JUN-2003; 2003GB-00015248.

XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.

XX Berndt P, Kilby PM, Rugman P;

XX WPI; 2005-050476/06.

PT New targets for an antiviral compound having at least one down- and up-  
 PT regulated hepatitis C virus (HCV) polypeptide, useful in predicting  
 PT outcomes, treating or preventing HCV infections.

XX Claim 1; SEQ ID NO 28; 346pp; English.

CC The invention comprises the amino acid sequences of protein targets for  
 CC anti-hepatitis C virus (anti-HCV) drugs. The human protein targets of the  
 CC invention are either up-regulated or down-regulated in HCV-infected  
 CC tissue. The proteins of the invention are useful in the preparation of a  
 CC medicament for the treatment or prevention of HCV infection. The present  
 CC amino acid sequence represents a human protein of the invention which is  
 CC down-regulated in HCV-infected tissue.

XX Sequence 458 AA;

Query Match 82.2%; Score 74; DB 9; Length 458;  
 Best Local Similarity 87.5%; Pred. No. 0.056;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1 LVVGLCTGQIKTGPAAC 16  
 |||||  
 Db 407 LVVGLCTGQIKTGPTC 422

RESULT 8  
 AAY43202  
 ID AAY43202 standard; peptide; 16 AA.

XX AAY43202;

XX 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #12.

KM Schizophrenic derived antibody; binding epitope; schizophrenia;  
 KM platelet-associated antibody; diagnosis.

OS Synthetic.

XX MO9951725-A2.

XX 14-OCT-1999.

XX 30-MAR-1999; 99WO-IL000190.

XX 02-APR-1998; 98IL-00123925.

XX (YEDA ) YEDA RES & DEV CO LTD.

XX Shinitzky M, Deckmann M;

XX WPI; 1999-611037/52.

PT New peptides useful for diagnosis of schizophrenia.

XX Claim 4; Page 21; 37pp; English.

CC This sequence is a peptide of the invention, which binds antibodies found  
 CC in elevated levels in body fluids of schizophrenic patients. The peptide  
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the  
 CC peptide to a platelet-containing fraction of blood, or a fraction  
 CC containing platelet-associated antibodies (PAA) shed from the platelets,  
 CC or preferably whole blood. The new peptides are able to differentiate  
 CC between plasma samples from schizophrenic and non-schizophrenic patients,  
 CC and can do so without having to first isolate the platelet-associated  
 CC antibodies (PAA) fraction

XX Sequence 16 AA;

Query Match 72.2%; Score 65; DB 2; Length 16;  
 Best Local Similarity 81.2%; Pred. No. 0.053;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Oy 1 LVVGLCTGQIKTGPAAC 16  
 |||||  
 Db 1 LVVGLCTGQIKTGPAAC 16

RESULT 9  
 AAY43196  
 ID AAY43196 standard; peptide; 17 AA.

XX AAY43196;

XX 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #6.

KM Schizophrenic derived antibody; binding epitope; schizophrenia;  
 KM platelet-associated antibody; diagnosis.

OS Synthetic.

XX MO9951725-A2.

XX 14-OCT-1999.

XX 30-MAR-1999; 99WO-IL000190.

XX 02-APR-1998; 98IL-00123925.

XX (YEDA ) YEDA RES & DEV CO LTD.

XX Shinitzky M, Deckmann M;

XX WPI; 1999-611037/52.

PT New peptides useful for diagnosis of schizophrenia.

XX Claim 3; Page 21; 37pp; English.

```
XX CC This sequence is a peptide of the invention, which binds antibodies found
CC in elevated levels in body fluids of schizophrenic patients. The peptide
CC is useful in an assay for the diagnosis of schizophrenia, by binding the
CC peptide to a platelet-containing fraction of blood, or a fraction
CC containing platelet-associated antibodies (PAA) shed from the platelets,
CC or preferably whole blood. The new peptides are able to differentiate
CC between plasma samples from schizophrenic and non-schizophrenic patients,
CC and can do so without having to first isolate the platelet-associated
CC antibodies (PAA) fraction
XX SQ Sequence 17 AA;

Query Match 72.2%; Score 65; DB 2; Length 17;
Best Local Similarity 81.2%; Pred. No. 0.056;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
DB 1 LVVGLCTGQIKTGAPC 16

RESULT 10
AAV43195
ID AAV43195 standard; peptide; 18 AA.
XX AAV43195;
AC
XX
XX 11-JAN-2000 (first entry)
DT
XX
XX Schizophrenic derived antibody binding epitope #5.
DE
XX
XX Schizophrenic derived antibody; binding epitope; schizophrenia;
KM platelet-associated antibody; diagnosis.
XX
XX Synthetic.
OS
XX WO9951725-A2.
PN
XX 14-OCT-1999.
PD
XX 30-MAR-1999; 99WO-IL000190.
PF
XX 02-APR-1998; 98IL-00123925.
PR
XX (YEDA ) YEDA RES & DEV CO LTD.
PA
XX Shintzky M, Deckmann M;
PI
XX
XX WPI; 1999-611037/52.
DR
XX
XX New peptides useful for diagnosis of schizophrenia.
PT
XX
XX Claim 3; Page 21; 37pp; English.
PS
XX
XX This sequence is a peptide of the invention, which binds antibodies found
CC in elevated levels in body fluids of schizophrenic patients. The peptide
CC is useful in an assay for the diagnosis of schizophrenia, by binding the
CC peptide to a platelet-containing fraction of blood, or a fraction
CC containing platelet-associated antibodies (PAA) shed from the platelets,
CC or preferably whole blood. The new peptides are able to differentiate
CC between plasma samples from schizophrenic and non-schizophrenic patients,
CC and can do so without having to first isolate the platelet-associated
CC antibodies (PAA) fraction
XX SQ Sequence 18 AA;

Query Match 72.2%; Score 65; DB 2; Length 18;
Best Local Similarity 81.2%; Pred. No. 0.059;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
DB 1 LVVGLCTGQIKTGAPC 16

RESULT 11
AAV43194
ID AAV43194 standard; peptide; 19 AA.
XX AAV43194;
AC
XX
XX 11-JAN-2000 (first entry)
DT
XX
XX Schizophrenic derived antibody binding epitope #4.
DE
XX
XX Schizophrenic derived antibody; binding epitope; schizophrenia;
KM platelet-associated antibody; diagnosis.
XX
XX Synthetic.
OS
XX WO9951725-A2.
PN
XX 14-OCT-1999.
PD
XX 30-MAR-1999; 99WO-IL000190.
PF
XX 02-APR-1998; 98IL-00123925.
PR
XX (YEDA ) YEDA RES & DEV CO LTD.
PA
XX Shintzky M, Deckmann M;
PI
XX
XX WPI; 1999-611037/52.
DR
XX
XX New peptides useful for diagnosis of schizophrenia.
PT
XX
XX Claim 3; Page 21; 37pp; English.
PS
XX
XX This sequence is a peptide of the invention, which binds antibodies found
CC in elevated levels in body fluids of schizophrenic patients. The peptide
CC is useful in an assay for the diagnosis of schizophrenia, by binding the
CC peptide to a platelet-containing fraction of blood, or a fraction
CC containing platelet-associated antibodies (PAA) shed from the platelets,
CC or preferably whole blood. The new peptides are able to differentiate
CC between plasma samples from schizophrenic and non-schizophrenic patients,
CC and can do so without having to first isolate the platelet-associated
CC antibodies (PAA) fraction
XX SQ Sequence 19 AA;

Query Match 72.2%; Score 65; DB 2; Length 19;
Best Local Similarity 81.2%; Pred. No. 0.062;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
DB 3 LVVGLCTGQIKTGAPC 18

RESULT 12
AAV43193
ID AAV43193 standard; peptide; 20 AA.
XX AAV43193;
AC
XX
XX 11-JAN-2000 (first entry)
DT
XX
XX Schizophrenic derived antibody binding epitope #3.
DE
XX
XX Schizophrenic derived antibody; binding epitope; schizophrenia;
KM platelet-associated antibody; diagnosis.
XX
XX Synthetic.
OS
XX WO9951725-A2.
PN
```

XX 14-OCT-1999.  
 XX 30-MAR-1999; 99WO-1L000190.  
 XX 02-APR-1998; 98IL-00123925.  
 XX (YEDA ) YEDA RES & DEV CO LTD.  
 XX Shinitzky M, Deckmann M;  
 XX WPI; 1999-611037/52.  
 XX New peptides useful for diagnosis of schizophrenia.  
 XX Claim 3; Page 21; 37pp; English.  
 CC This sequence is a peptide of the invention, which binds antibodies found  
 CC in elevated levels in body fluids of schizophrenic patients. The peptide  
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the  
 CC peptide to a platelet-containing fraction of blood, or a fraction  
 CC containing platelet-associated antibodies (PAA) shed from the platelets,  
 CC or preferably whole blood. The new peptides are able to differentiate  
 CC between plasma samples from schizophrenic and non-schizophrenic patients,  
 CC and can do so without having to first isolate the platelet-associated  
 CC antibodies (PAA) fraction  
 CC  
 SQ Sequence 20 AA:

Query Match 72.2%; Score 65; DB 2; Length 20;  
 Best Local Similarity 81.2%; Pred. No. 0.064;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGPAC 16  
 |||||  
 Db 4 LVVGLCTGQIKTGAPC 19

## RESULT 13

AAV43192  
 ID AAV43192 standard; peptide; 28 AA.

AC AAV43192;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #2.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;  
 platelet-associated antibody; diagnosis.

OS Synthetic.

XX WO9951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-1L000190.

PR 02-APR-1998; 98IL-00123925.

PA (YEDA ) YEDA RES & DEV CO LTD.

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

CC New peptides useful for diagnosis of schizophrenia.

PS Claim 3; Page 21; 37pp; English.

CC This sequence is a peptide of the invention, which binds antibodies found  
 CC in elevated levels in body fluids of schizophrenic patients. The peptide

CC is useful in an assay for the diagnosis of schizophrenia, by binding the  
 CC peptide to a platelet-containing fraction of blood, or a fraction  
 CC containing platelet-associated antibodies (PAA) shed from the platelets,  
 CC or preferably whole blood. The new peptides are able to differentiate  
 CC between plasma samples from schizophrenic and non-schizophrenic patients,  
 CC and can do so without having to first isolate the platelet-associated  
 CC antibodies (PAA) fraction  
 CC  
 SQ Sequence 28 AA:

Query Match 72.2%; Score 65; DB 2; Length 28;  
 Best Local Similarity 81.2%; Pred. No. 0.086;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGPAC 16  
 |||||  
 Db 12 LVVGLCTGQIKTGAPC 27

## RESULT 14

ID ADU78952 standard; protein; 50 AA.

AC ADU78952;

DT 27-JAN-2005 (first entry)

DE Human protein fragment, SEQ ID 325.

KW Neuroprotective; Antidepressant; Neuroleptic; Tranquillizer;  
 Antiparkinsonian; Nootropic; Antidiabetic; Anorectic;

KW Cardiovascular-Gen.; Antiartherosclerotic; Antilipemic;  
 Alzheimer's disease; neurological disorder; phosphatase; enzyme.

OS Homo sapiens.

XX US2004226056-A1.

PD 11-NOV-2004.

PF 09-FEB-2004; 2004US-00776013.

PR 22-DEC-1998; 98US-0113534P.

PR 12-MAR-1999; 99US-0124120P.

PR 30-JUN-1999; 99US-0141243P.

PR 21-DEC-1999; 99US-0046613P.

PR 17-OCT-2000; 2000US-0240790P.

PR 13-JUL-2001; 2001US-0304775P.

PR 10-SEP-2001; 2001US-00948904.

PR 12-OCT-2001; 2001US-00975072.

PR 15-JUL-2002; 2002US-00194967.

PA (MYRIAD GENETICS INC.

PI Roch J, Bartel P, Heichman K;

DR WPI; 2004-794772/78.

CC Selecting agents useful for treating Alzheimer's disease comprises  
 CC contacting focal adhesion kinase 2 with a test agent and measuring a  
 CC biological activity related to focal adhesion kinase 2 function with or  
 CC without the test agent.

CC Disclosure; SEQ ID NO 325; 247pp; English.

CC The present invention relates to a method for selecting agents that are  
 CC potentially useful for the treatment of Alzheimer's disease. The method  
 CC comprises contacting Focal Adhesion Kinase 2 (FAK2) with a test agent and  
 CC measuring a biological activity related to FAK2 function in the presence  
 CC and absence of the test agent. The method is useful for screening  
 CC compounds or agents that can be used to treat neurological disorders,  
 CC ailments and diseases including mild cognitive impairment, depression,  
 CC schizophrenia, obsessive-compulsive disorder, bipolar disorder, and





CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 269 AA;

Query Match 72.2%; Score 65; DB 6; Length 269;  
Best Local Similarity 81.2%; Pred. No. 0.6;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGAPAC 16  
Db 219 LVVGLCTGQIKTGAPC 234

RESULT 17  
ADZ70357  
ID ADZ70357 standard; protein; 269 AA.

AC ADZ70357;  
DT 30-JUN-2005 (first entry)

DE Human protein from lung cancer marker gene ENOL, SEQ ID 42.

KW Tumor marker; lung tumor; cytostatic; neoplasm; expression;  
KW DNA microarray.

XX Homo sapiens.

PN WO2005032495-A2.

PD 14-APR-2005.

PF 01-OCT-2004; 2004WO-US034163.

PR 03-OCT-2003; 2003US-0508355P.

PA (FARB ) BAYER PHARM CORP.

PI Taylor I, Pauloski NR, Bigwood D;

XX WPI; 2005-285325/29.

DR N-PSDB; ADZ70356.

XX Providing a patient diagnosis for lung cancer comprises comparing the  
PT level of expression of genes or gene products in a biological sample from  
PT the patient with that from a normal individual.

XX Claim 3; SEQ ID NO 42; 60pp; English.

PS The invention relates to providing a patient diagnosis for lung cancer  
CC comprising comparing the level of expression of genes or gene products in  
CC a biological sample from the patient with the level of expression of  
CC genes or gene products in a biological sample from a normal individual.  
CC Also included are distinguishing between normal and disease tissues,  
CC monitoring the response of a patient being treated for lung cancer by  
CC administering an anti-cancer agent, identifying a compound useful for the  
CC treatment of lung cancer and an array for distinguishing between normal  
CC and disease tissues (comprising 2 or more probes corresponding to 2 or  
CC more genes selected from any of the 200 nucleotide sequences given in the  
CC specification, or 2 or more polypeptides comprising any of the 200 amino  
CC acid sequences given in the specification). In providing a patient  
CC diagnosis for lung cancer, one or more genes are selected from any of the  
CC 200 nucleotide sequences as mentioned in the specification, or one or  
CC more gene products are polypeptides selected from any of the 20 amino  
CC acid sequences mentioned in the specification. The methods are useful for  
CC detecting and treating lung cancer. These may also be used for designing,  
CC identifying and optimizing therapeutics for cancer. The present sequence  
CC represents a protein from one of the 200 lung cancer marker genes. Note:

CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 269 AA;

Query Match 72.2%; Score 65; DB 9; Length 269;  
Best Local Similarity 81.2%; Pred. No. 0.6;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGAPAC 16  
Db 219 LVVGLCTGQIKTGAPC 234

RESULT 18  
ABU04378  
ID ABU04378 standard; protein; 272 AA.

AC ABU04378;

DT 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1044.

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW proteinase; proteinase inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

PN WO200278524-A2.

PD 10-OCT-2002.

PF 28-MAR-2002; 2002WO-US009671.

PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCO INC.

PA Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.

XX Example 2; SEQ ID NO 1044; 134pp; English.

PS The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational

CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

SO Sequence 272 AA;

Query Match 72.2%; Score 65; DB 6; Length 272;  
Best Local Similarity 81.2%; Pred. No. 0.61;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
Db 222 LVVGLCTGQIKTGAPC 237

RESULT 19  
ABU04375  
ID ABU04375 standard; protein; 272 AA.  
XX  
AC ABU04375;

DT 29-JAN-2003 (first entry)  
XX

DE Human expressed protein tag (EPT) #1041.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.

OS Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0292544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

XX Chicz RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
XX leukemia.

PS Example 2; SEQ ID NO 1041; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational

CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

SO Sequence 272 AA;

Query Match 72.2%; Score 65; DB 6; Length 272;  
Best Local Similarity 81.2%; Pred. No. 0.61;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
Db 222 LVVGLCTGQIKTGAPC 237

RESULT 20  
ABU04376  
ID ABU04376 standard; protein; 336 AA.  
XX  
AC ABU04376;

DT 29-JAN-2003 (first entry)  
XX

DE Human expressed protein tag (EPT) #1042.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.

OS Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0292544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

XX Chicz RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
XX leukemia.

PS Example 2; SEQ ID NO 1042; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational

CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

SO Sequence 336 AA;

Query Match 72.2%; Score 65; DB 6; Length 336;  
Best Local Similarity 81.2%; Pred. No. 0.73;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 286 LVVGLCTGQIKTGAPC 301

RESULT 21

ID AAE38225 standard; protein; 420 AA.

AC AAE38225;

DT 20-NOV-2003 (first entry)

DE Human enzyme (ENZY) protein #17.

KW Human; enzyme; ENZY; immune disorder; infection; myocardial infarction;  
KW gene therapy; anaemia; acquired immune deficiency syndrome; infection;  
KW reproductive disorder; cardiovascular; eye; cell proliferation; cancer;  
KW AIDS; allergy; asthma; Addison's disease; diabetes; goitre; impotence;  
KW infertility; atherosclerosis; metabolic disorder.

OS Homo sapiens.

PN WO2003052075-A2.

PD 26-JUN-2003.

PF 12-DEC-2002; 2002WO-US040161.

PR 14-DEC-2001; 2001US-0340357P.

PR 20-DEC-2001; 2001US-0342962P.

PR 21-DEC-2001; 2001US-0343558P.

PR 22-JAN-2002; 2002US-0351107P.

XX (INCY-) INCYTE GENOMICS INC.

PI Chawla NK, Lee SY, Ring HZ, Lee EA, Forsythe ID, Khare R;  
PI Tran UK, Kabie AE, Richardson TW, Emerling BM, Lindquist EA;  
PI Baughn MR, Hafalla AJA, Jin P, Swarnakar A, Li JX, Margulis JP;  
PI Lee S, Gorvad AE, Sprague WW, Becha SD, Elliott VS;

XX WPI; 2003-533016/50.

DR N-PSDB; AAD57505.

PT New human enzyme (ENZY) polypeptide, useful for preparing a composition  
PT for treating a disease associated with decreased expression or  
PT overexpression of ENZY e.g. cancer.

XX Claim 1; Page 283; 264pp; English.

XX The invention relates to human enzyme (ENZY) polypeptides and their  
XX corresponding polynucleotides. ENZY sequences are useful for preparing a  
XX composition for diagnosing or treating a disease or condition associated  
XX with decreased expression or overexpression of functional ENZY. The  
XX disorders include immune disorders (anaemia, allergy or asthma),  
XX infectious disorders (viral, fungal, parasitic or protozoal infection),  
XX immune deficiencies (acquired immune deficiency syndrome; AIDS),  
XX metabolic disorder (Addison's disease, diabetes or goitre), reproductive  
XX disorders (infertility or impotence), cardiovascular disorders  
XX (atherosclerosis or myocardial infarction), eye disorders and cell  
XX proliferative disorders (cancer). ENZY DNA is useful in gene therapy. The  
XX present sequence is human ENZY protein

SO Sequence 420 AA;

Query Match 72.2%; Score 65; DB 6; Length 420;  
Best Local Similarity 81.2%; Pred. No. 0.88;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 370 LVVGLCTGQIKTGAPC 385

RESULT 22

ID AAB42064 standard; protein; 429 AA.

AC AAB42064;

DT 08-FEB-2001 (first entry)

DE Human ORFX ORF1828 polypeptide sequence SEQ ID NO:3656.

KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;  
KW vulnery; antiproliferative; antiparkinsonian; neurotrophic; neuroprotective;  
KW anticonvulsant; osteopachic; antiarthritic; immunosuppressant; cardiant;  
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;  
KW antiviral; antibacterial; antifungal; antineumatic; antithyroid;  
KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;  
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
KW cardiovascular disease; diabetes mellitus; hypochyroidism; SCID; AIDS;  
KW cholesterol ester storage; systemic lupus erythematosus; infection;  
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;  
KW thrombosis; contraceptive.

OS Homo sapiens.

PN WO200058473-A2.

PD 05-OCT-2000.

PF 31-MAR-2000; 2000WO-US008621.

PR 31-MAR-1999; 99US-0127607P.

PR 02-APR-1999; 99US-0127636P.

PR 05-APR-1999; 99US-0127728P.

PR 30-MAR-2000; 2000US-00540763.

XX (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M;

XX WPI; 2000-602362/57.

DR N-PSDB; AAC76273.

PT Novel nucleic acids and peptides derived from open reading frame X,  
PT useful for treating e.g. cancers, proliferative disorders,  
PT neurodegenerative disorders and cardiovascular disease.

XX Claim 11; Page 2810-2811; 5507pp; English.

XX AACT74446 to AACT7606 encode the proteins given in AAB40237 to AAB43397,  
XX which represent the human ORFX open reading frames 1 to 3161. The ORFX  
XX sequences have activities such as: cytostatic; hepatotropic; vulnery;  
XX antiproliferative; antiparkinsonian; neurotrophic; neuroprotective; osteopachic;  
XX anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;  
XX cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;  
XX dermatological; immunosuppressive; antiinflammatory; antibacterial;  
XX antiviral; antifungal; antineumatic; antithyroid; and antianemic. The  
XX sequences can be used for determining the presence of or predisposition  
XX to, or preventing or treating pathological conditions associated with an  
XX ORFX-associated disorder. The nucleic acids can be used to express ORFX



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DB      383 LVVGLCTGQIKTGAPC 398

RESULT 25
AAW54357
ID      AAW54357 standard; protein; 433 AA.
XX      AAW54357;
AC      AAW54357;
XX      14-AUG-1998 (first entry)
XX      Alpha Enolase.
DE      Endometrium; hyperplasia; adenocarcinoma; proliferative phase;
KM      2D gel electrophoresis; detection.
XX      Homo sapiens.
OS      WO9810291-A1.
XX      12-MAR-1998.
PD      05-SEP-1997; 97WO-GB002394.
XX      06-SEP-1996; 96GB-00018600.
PR      08-APR-1997; 97GB-00007132.
XX      (CLIN-) CENT CLINICAL & BASIC RES.
XX      PA
XX      Byrjalsen I, Larsen P, Fey SJ;
PI      WPI; 1998-207057/18.
XX      Biochemical markers of human endometrium - useful for, e.g. diagnosis of
XX      hyperplasia and adenocarcinoma.
XX      Disclosure; Page 21, 77pp; English.
XX      Proteins AAW54349-W54364 are examples of proteins produced in the
XX      endometrium during the hyperplasia, adenocarcinoma or proliferative phase
XX      of the endometrium. The presence and quantities of these proteins can be
XX      detected using 2D gel electrophoresis comparison of cell lysates. The
XX      proteins can be used as biochemical markers to detect the phase of the
XX      endometrium and can be measured in body fluids, obviating the need for
XX      endometrial biopsies
XX      SQ
XX      Sequence 433 AA:

Query Match      72.2%; Score 65; DB 2; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.9;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 LVVGLCTGQIKTGAPC 16
        |||||
DB      383 LVVGLCTGQIKTGAPC 398

RESULT 26
ABU03944
ID      ABU03944 standard; protein; 433 AA.
XX      ABU03944;
AC      ABU03944;
XX      29-JAN-2003 (first entry)
XX      Human expressed protein tag (EPT) #610.
XX      Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM      protease; protease inhibitor; transporter; cytoskeletal protein;
XX      receptor; transcription factor; cancer; MHC;
XX      major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM      adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX

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OS	Homo sapiens.
XX	
PN	WO200278524-A2.
XX	
PD	10-OCT-2002.
XX	
PE	28-MAR-2002; 2002WO-US009671.
XX	
PR	28-MAR-2001; 2001US-0279495P.
PR	21-MAY-2001; 2001US-0292544P.
PR	08-AUG-2001; 2001US-0310801P.
PR	01-OCT-2001; 2001US-0326370P.
PR	04-DEC-2001; 2001US-0336780P.
PR	20-FEB-2002; 2002US-0358985P.
XX	
PA	(ZYCO-) ZYCOS INC.
XX	
PI	Chicz RM, Tomlinson AJ, Urban RG;
XX	
DR	WPI; 2003-040607/03.
XX	
PT	New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.
PT	
XX	
PS	Example 2; SEQ ID NO 610; 134pp; English.
XX	
CC	The invention describes a purified polypeptide, which comprises a
CC	fragment of a kinase, phosphatase, protease, protease inhibitor,
CC	transporter, cytoskeletal protein, receptor or transcription factor. The
CC	polypeptide is useful as an immunogenic composition for eliciting in a
CC	mammal an immunogenic response directed against any of the purified
CC	polypeptide. The purified polypeptide, or the antibody that binds to this
CC	polypeptide, is useful for treating cancer. The polypeptide is also
CC	useful for identifying compounds that binds to a naturally processed
CC	class I or class II MHC-binding polypeptide. The polypeptides and
CC	polynucleotides are particularly useful for treating or preventing
CC	myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC	lymphoma or leukaemia. These are also useful for screening agents for
CC	treating the above mentioned diseases. This sequence represents an
CC	expressed protein tag (EPT) isolated from human tissue for translational
CC	profiling. Note: This sequence does not appear in the printed
CC	specification but was obtained in electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
SO	Sequence 433 AA;
XX	
Query Match	72.2%; Score 65; DB 6; Length 433;
Best Local Similarity	81.2%; Pred. No. 0.9;
Matches	13; Conservative 0; Mismatches 3; Indels 0; Gaps 0
QY	1 LVVGLCTCQIKTGPAC 16
DB	383 LVVGLCTCQIKTGPAC 398
XX	
RESULT 27	
ABU03942	
ID	ABU03942 standard; protein; 433 AA.
XX	
AC	ABU03942;
XX	
DT	29-JAN-2003 (first entry)
XX	
DE	Human expressed protein tag (EPT) #608.
XX	
KW	Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW	protease; protease inhibitor; transporter; cytoskeletal protein;
KW	receptor; transcription factor; cancer; MHC;
KW	major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW	adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX	

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OS Homo sapiens.
XX
XX WO200278524-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
XX 21-MAY-2001; 2001US-0292544P.
XX 08-AUG-2001; 2001US-0310801P.
XX 01-OCT-2001; 2001US-0326370P.
XX 04-DEC-2001; 2001US-0336780P.
XX 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX
XX Example 2; SEQ ID NO 608; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (Ept) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 433 AA;
XX
XX Query Match 72.2%; Score 65; DB 6; Length 433;
XX Best Local Similarity 81.2%; Pred. No. 0.9;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 LVVGLCTGQIKTGAPC 16
XX |||||
XX Db 383 LVVGLCTGQIKTGAPC 398
XX
XX RESULT 28
XX ID ADQ30574 standard; protein; 433 AA.
XX
XX AC ADQ30574;
XX
XX DT 23-SEP-2004 (first entry)
XX
XX DE Pancreas cancer marker - human alpha enolase.
XX
XX KW Cytostatic; diagnosis; pancreatic cancer; antibody; antisense construct;
XX differential expression.
XX
XX OS Homo sapiens.
XX
XX WO2004055519-A2.
```

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XX
XX 01-JUL-2004.
XX
XX PD 11-DEC-2003; 2003WO-EP014057.
XX
XX PR 17-DEC-2002; 2002EP-00028058.
XX
XX PR 05-NOV-2003; 2003EP-00025237.
XX
XX (HOFF) HOFFMANN LA ROCHE & CO AG P.
XX (SINO-) SINGENOMAX CO LTD CHINESE NAT HUMAN GEN.
XX
XX PI Chen J, Hu L, Liu TH, Lu ZH, Shen Y;
XX
XX WPI; 2004-488121/46.
XX
XX New specific markers comprises at least one polypeptide up-regulated in
XX pancreatic cancer, useful for diagnosing pancreatic cancer.
XX
XX PS Claim 1; SEQ ID NO 61; 381pp; English.
XX
XX The invention relates to a marker (I) for diagnosis of pancreatic cancer
XX comprising at least one polypeptide selected from 55 proteins up-
XX regulated in pancreatic cancer (Table 2 and Table 3, given in the
XX specification) or from 68 proteins with higher levels in pancreatic
XX cancer compared to normal tissue (Table 6, given in the specification).
XX (I) is a polypeptide for use as a marker or as a component of a marker
XX for diagnosis of pancreatic cancer and/or the susceptibility to
XX pancreatic cancer. A compound (antibody, an antibody-derivative, an
XX antibody fragment, a peptide, or an antisense construct) identified by
XX screening methods using (I) is useful for treatment or prevention of
XX pancreatic cancer. It is also useful for the preparation of a diagnostic
XX composition for diagnosing pancreatic cancer or a predisposition for
XX pancreatic cancer. The current polypeptides were found to be
XX differentially expressed in pancreatic tissue obtained from individuals
XX suffering from pancreatic cancer as compared to healthy pancreatic
XX tissue. They have been identified as suitable as markers of pancreatic
XX cancer for early diagnosis of the disease. This sequence corresponds to a
XX protein marker of the invention.
XX
XX SQ Sequence 433 AA;
XX
XX Query Match 72.2%; Score 65; DB 8; Length 433;
XX Best Local Similarity 81.2%; Pred. No. 0.9;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 LVVGLCTGQIKTGAPC 16
XX |||||
XX Db 383 LVVGLCTGQIKTGAPC 398
XX
XX RESULT 29
XX ID ABB57379 standard; protein; 434 AA.
XX
XX AC ABB57379;
XX
XX DT 07-AUG-2003 (revised)
XX DT 08-MAR-2002 (first entry)
XX
XX DE Rat mucocardial cell proliferation associated polypeptide SEQ ID NO 10.
XX
XX KW Rat; heart; cardiast; myocardial necrosis; cardiac hypertrophy;
XX cardiac insufficiency.
XX
XX OS Rattus norvegicus.
XX
XX WO200183705-A1.
XX
XX PD 08-NOV-2001.
XX
XX PF 27-APR-2001; 2001WO-JP003700.
XX
XX PR 27-APR-2000; 2000JP-00126741.
```

XX (KYOW) KYOWA HAKKO KOGYO KK.  
 PA Yamada Y, Sekine S, Kikuchi Y, Sakurada K;  
 PI WPI, 2002-075160/10.  
 DR N-PSDB; ABI99919.  
 XX  
 PT Genes having differential expression in fetal and adult heart tissue  
 PT caused by myocardial necrosis.  
 PT  
 PS Claim 53; Page 98-100; 171pp; Japanese.  
 CC The invention relates to gene sequences (ABI99915-ABI99934) having  
 CC modified expression in fetal heart tissue as compared to adult heart  
 CC tissue and the encoded proteins (ABBS7375-ABBS7392). The genes have  
 CC cardiant activity and may be useful in the promotion of the repair of  
 CC damage to heart tissue caused by myocardial necrosis. The gene sequences  
 CC are useful for screening potential compounds for the ability to influence  
 CC disease associated with myocardial necrosis. Drugs identified by the  
 CC screening methods may be used to treat and prevent disease with which  
 CC myocardial necrosis is associated, such as cardiac hypertrophy and  
 CC cardiac insufficiency. Diagnosis of diseases such as those above is also  
 CC disclosed. (Updated on 07-AUG-2003 to correct OS field.)  
 CC  
 SO Sequence 434 AA;  
 SQ  
 Query Match 72.2%; Score 65; DB 5; Length 434;  
 Best Local Similarity 81.2%; Pred. No. 0.91;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 LVVGLCTGQIKTGAPC 16  
 DB 384 LVVGLCTGQIKTGAPC 399  
 RESULT 30  
 ID ABP65147 standard; protein; 434 AA.  
 AC ABP65147;  
 XX  
 DT 12-NOV-2002 (first entry)  
 XX  
 DE Hypoxia-regulated protein #21.  
 XX  
 KW Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy;  
 KW antiinflammatory; vulnerrary; gynecological; ophthalmological; vaccine;  
 KW hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer;  
 KW ischaemic condition; reperfusion injury; retinopathy; neonatal stress;  
 KW preclapmsia; atherosclerosis; inflammatory condition; wound healing;  
 KW inflammation; erythropoiesis; hair loss; human.  
 XX  
 OS Homo sapiens.  
 PN WO200246465-A2.  
 XX  
 PD 13-JUN-2002.  
 XX  
 PF 10-DEC-2001; 2001WO-GB005458.  
 XX  
 PR 08-DEC-2000; 2000GB-00030076.  
 PR 08-EB-2001; 2001GB-0003156.  
 PR 25-OCT-2001; 2001GB-00025666.  
 XX  
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
 XX  
 PI White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;  
 PI Rayner WN;  
 XX  
 DR WPI, 2002-627238/67.  
 XX

PT Identifying a gene involved in disease for treating hypoxia-regulated  
 PT conditions, comprises comparing the transcriptome/proteome of two cell  
 PT types under different conditions and identifying a differentially  
 PT regulated gene.  
 PS Claim 35; Page 344; 538pp; English.  
 CC  
 CC The present invention relates to methods for identifying genes and  
 CC proteins that are implicated in a specific disease or physiological  
 CC condition. The method comprises comparing the transcriptome/proteome of a  
 CC specialised cell type implicated in a disease or condition with that of a  
 CC second specialised cell type, under two experimental conditions, and  
 CC identifying a gene that is differentially regulated in the two  
 CC specialised cell types under experimental conditions. ABV7873-ABV78116  
 CC and ABP65061-ABP65257 were identified using the methods of the invention.  
 CC The coding sequences and proteins are useful for treating a disease in a  
 CC patient, for manufacture of a medicament for treating hypoxia-regulated  
 CC conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,  
 CC biological response to hypoxia conditions, or hypoxic-associated  
 CC pathology in a patient. The coding sequences and proteins are also useful  
 CC for monitoring the therapeutic treatment of a disease or physiological  
 CC condition, such as cancer, ischaemic conditions, reperfusion injury,  
 CC retinopathy, neonatal stress, preclapmsia, atherosclerosis, inflammatory  
 CC conditions, wound healing, inflammation, erythropoiesis or hair loss  
 CC  
 SO Sequence 434 AA;  
 SQ  
 Query Match 72.2%; Score 65; DB 5; Length 434;  
 Best Local Similarity 81.2%; Pred. No. 0.91;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 LVVGLCTGQIKTGAPC 16  
 DB 384 LVVGLCTGQIKTGAPC 399

Search completed: April 3, 2006, 08:04:17  
 Job time : 85 secs

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## ALIGNMENTS

RESULT 1  
137360 phosphopyruvate hydratase (EC 4.2.1.11), lung - human  
N/Alternate names: enolase  
C/Species: Homo sapiens (man)  
C/Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004  
C/Accession: 137360; S22071  
R/Yerna, M.; Kurl, R.N.  
Biochem. Inc. 30, 293-303, 1993  
A/Title: Human lung enolase: cloning and sequencing of cDNA and its inducibility with de  
A/Reference number: 137360  
A/Accession: 137360  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-458 <VER>  
A/Cross-references: UNIPROT:005524; UNIPARC:UPI0000129F55; EMBL:X6610; NID:g31178; PIDN  
A/Note: submitted to the EMBL Data Library, June 1992  
C/Function:  
A/Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phos  
C/Pathway: gluconeogenesis; glycolysis  
C/Superfamily: enolase  
C/Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesium  
F/43/Binding site: magnesium 2 (Set) #status predicted  
F/219/Active site: Glu, Lys #status predicted  
F/254,308,336/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 82.2%; Score 74; DB 2; Length 458;  
Best Local Similarity 87.5%; Pred. No. 0.00059;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 407 LVVGLCTGQIKTGPTC 422

RESULT 2  
150026 phosphopyruvate hydratase (EC 4.2.1.11) alpha - American alligator (fragment)  
N/Alternate names: alpha-enolase  
C/Species: Alligator mississippiensis (American alligator)  
C/Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 09-Jul-2004  
C/Accession: 150026  
R/Hedger, S.B.  
Proc. Natl. Acad. Sci. U.S.A. 91, 2621-2624, 1994  
A/Title: Molecular evidence for the origin of birds.  
A/Reference number: A53470; MUID:94195794; PMID:8146164  
A/Accession: 150026  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown; translate  
A/Molecule type: mRNA  
A/Residues: 1-395 <HED>  
A/Cross-references: UNIPROT:P42897; UNIPARC:UPI0000129F57; GB:I28078; NID:g472796; PIDN:  
A/Superfamily: enolase  
C/Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 72.2%; Score 65; DB 2; Length 395;  
Best Local Similarity 81.2%; Pred. No. 0.013;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 362 LVVGLCTGQIKTGAPC 377

RESULT 3  
A37210 phosphopyruvate hydratase (EC 4.2.1.11) beta - rabbit  
N/Alternate names: enolase beta  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 05-Oct-2004  
C/Accession: A37210

R/Chin, C.C.Q.  
J. Protein Chem. 9, 427-432, 1990  
A/Title: The primary structure of rabbit muscle enolase.  
A/Reference number: A37210; MUID:91113295; PMID:2275753  
A/Accession: A37210  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-433 <CHI>  
A/Cross-references: UNIPROT:P25704; UNIPARC:UPI000017606F  
C/Superfamily: enolase  
C/Keywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase  
F/1/Modified site: acetylated amino end (Ala) #status experimental

Query Match 72.2%; Score 65; DB 2; Length 433;  
Best Local Similarity 81.2%; Pred. No. 0.014;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 383 LVVGLCTGQIKTGAPC 398

RESULT 4  
NOHUG  
phosphopyruvate hydratase (EC 4.2.1.11) gamma - human  
N/Alternate names: enolase gamma; neuron-specific enolase  
C/Species: Homo sapiens (man)  
C/Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 05-Oct-2004  
C/Accession: J00060; S16163; S02077; S56569; S02616; S38303  
R/Oliva, D.; Barba, G.; Barberi, G.; Giallongo, A.; Feo, S.  
Gene 79, 355-360, 1989  
A/Title: Cloning, expression and sequence homologies of cDNA for human gamma enolase.  
A/Reference number: J00060; MUID:9006764; PMID:2792767  
A/Accession: J00060  
A/Molecule type: mRNA  
A/Residues: 1-434 <OLI>  
A/Cross-references: UNIPROT:P09104; UNIPARC:UPI000013C8F1; GB:M22349; NID:g951199; PIDN  
R/Oliva, D.; Cali, L.; Feo, S.; Giallongo, A.  
Genomics 10, 157-165, 1991  
A/Title: Complete structure of the human gene encoding neuron-specific enolase.  
A/Reference number: S16163; MUID:91257823; PMID:2045099  
A/Accession: S16163  
A/Molecule type: DNA  
A/Residues: 1-434 <OLI>  
A/Cross-references: UNIPARC:UPI000013C8F1; GB:X51956; NID:g31164; PIDN:CAA36215.1; PID:  
R/McLese, S.M.; Dunbar, B.; Fothergill, J.E.; Hinks, L.J.; Day, I.N.M.  
Eur. J. Biochem. 178, 413-417, 1988  
A/Title: Complete amino acid sequence of the neuron-specific gamma isozyme of enolase  
A/Reference number: S02077; MUID:89091176; PMID:3208766  
A/Accession: S02077  
A/Molecule type: mRNA  
A/Residues: 2-3, 'Q', 'S', '239', 'W', '241-434' <MCA>  
A/Cross-references: UNIPARC:UPI000015B77; EMBL:X13120; NID:g31145; PIDN:CAA31512.1; PI  
A/Note: part of this sequence was confirmed by protein sequencing  
A/Note: 264-Ala and 395-Ala were also found  
R/Van Obergerghen, E.; Kamholz, J.; Bishop, J.G.  
J. Neurosci. Res. 19, 450-456, 1988  
A/Title: Human gamma enolase: isolation of a cDNA clone and expression in normal and tum  
A/Reference number: S56569; MUID:88299288; PMID:3385803  
A/Accession: S56569  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 'GC', '29-126', 'N', '128-434' <VAN>  
A/Cross-references: UNIPARC:UPI000016A897; GB:M36768; NID:g182117; PIDN:AAA52388.1; PID:  
R/Day, I.N.M.; Allsopp, M.T.E.P.; Moore, D.C.M.; Thompson, R.J.  
FEBS Lett. 222, 139-143, 1987  
A/Title: Sequence conservation in the 3'-untranslated regions of neuron-specific enolase  
A/Reference number: S02616; MUID:88005129; PMID:3653393  
A/Accession: S02616  
A/Status: not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 425-434 <DAV>  
A/Cross-references: UNIPARC:UPI0000172FAB; GB:X00691; GB:M27610

R.Harrington, C.R.; Quinn, G.B.; Hurt, J.; Day, I.N.M.; Wischik, C.M.  
 Biochim. Biophys. Acta 1158, 120-128, 1993  
 A>Title: Characterisation of an epitope specific to the neuron-specific isoform of human  
 of beta/A4-protein.  
 A:Reference number: S38303; MUID:94002176; PMID:7691181  
 A:Accession: S38303  
 A:Molecule type: protein  
 A:Residues: 156-173 <HAR>  
 A:Cross-references: UNIPARC:UPI0000172PAC  
 C:Comment: Enolase occurs with at least three isoforms (alpha, beta, and gamma) in mamma  
 C:Comment: Thr-191 may be important for the enhanced tolerance to chloride ions of neuro  
 C:Genetics:  
 A:Gene: GDB:EMO2  
 A:Cross-references: GDB:119872; OMIM:131360  
 A:Map position: 12p13-12p13  
 A:Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/2; 412/2  
 C:Function:  
 C:Complex: homodimer  
 A:Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phos  
 A:Pathway: gluconeogenesis; glycolysis  
 C:Superfamily: enolase  
 C:Keywords: blocked amino end; brain; carbon-oxygen lyase; gluconeogenesis; glycolysis;  
 F:2-434/Product: phosphopyruvate hydratase gamma #status predicted <MAT>  
 F:2/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #statu  
 F:40/Binding site: magnesium 2 (Ser) #status predicted  
 F:210,343/Active site: Glu, Lys #status predicted  
 F:245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 72.2%; Score 65; DB 1; Length 434;  
 Best Local Similarity 81.2%; Pred. No. 0.014;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTQIKTGAPC 16  
 DB 384 LVVGLCTQIKTGAPC 399

RESULT 5  
 NOMSB  
 phosphopyruvate hydratase (EC 4.2.1.11) beta - mouse  
 N:Alternate names: enolase beta  
 C:Species: Mus musculus (house mouse)  
 C:Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text\_change 05-Oct-2004  
 C:Accession: S17109; S18036; S29675; A33921  
 R:Landmark, N.; Brosset, S.; Keller, A.; Lucas, M.; Lazar, M.  
 Submitted to the EMBL Data Library, September 1991  
 A:Reference number: S17109  
 A:Accession: S17109  
 A:Molecule type: DNA  
 A:Residues: 1-434 <LAM>  
 A:Cross-references: UNIPROT:P21550; UNIPARC:UPI0000001937; EMBL:X61600; NID:G50848; PIDN  
 R:Peterson, C.A.; Cho, M.; Rastinejad, F.; Blau, H.M.  
 Submitted to the EMBL Data Library, October 1991  
 A:Description: Beta-enolase: a gene expressed in undifferentiated postnatal myoblasts th  
 A:Reference number: S18036  
 A:Accession: S18036  
 A:Molecule type: mRNA  
 A:Residues: 1-434 <PET>  
 A:Cross-references: UNIPARC:UPI0000001937; EMBL:X62667; NID:G50143; PIDN:CAA44540.1; PID  
 R:Lazar, M.; Landmark, N.; Brosset, S.; Lucas, M.; Keller, A.  
 Submitted to the EMBL Data Library, February 1991  
 A:Reference number: S29675  
 A:Accession: S29675  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-434 <LAZ>  
 A:Cross-references: UNIPARC:UPI0000001937; EMBL:S57747; NID:G50846; PIDN:CAA40913.1; PID  
 R:Landmark, N.; Maza, A.M.; Lucas, M.; Montarras, D.; Pinset, C.; Gros, F.; Legault-Demar  
 Proc. Natl. Acad. Sci. U.S.A. 86, 4445-4449, 1989  
 A>Title: Murine muscle-specific enolase: cDNA cloning, sequence, and developmental expre  
 A:Reference number: A33921; MUID:89282789; PMID:2734297  
 A:Accession: A33921  
 A:Status: preliminary

A:Molecule type: mRNA  
 A:Residues: 59-233 'NA' 236-434 <LA2>  
 A:Cross-references: UNIPARC:UPI000016C036; GB:M20745; NID:G193029; PIDN:AAA37554.1; PI  
 A:Experimental source: skeletal muscle  
 C:Genetics:  
 A:Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2  
 C:Function:  
 A:Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to ph  
 A:Pathway: gluconeogenesis; glycolysis  
 C:Superfamily: enolase  
 C:Keywords: carbon-carbon lyase; carbon-oxygen lyase; dimer; gluconeogenesis; glycolys  
 F:40/Binding site: magnesium 2 (Ser) #status predicted  
 F:210,343/Active site: Glu, Lys #status predicted  
 F:245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 72.2%; Score 65; DB 1; Length 434;  
 Best Local Similarity 81.2%; Pred. No. 0.014;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTQIKTGAPC 16  
 DB 384 LVVGLCTQIKTGAPC 399

RESULT 6  
 NOXL  
 phosphopyruvate hydratase (EC 4.2.1.11) ENO1 - African clawed frog  
 N:Alternate names: enolase ENO1  
 C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 31-Mar-1991 #sequence revision 31-Mar-1991 #text\_change 05-Oct-2004  
 C:Accession: S00463  
 R:Segall, N.; Shrutkowski, A.; Dworkin, M.B.; Dworkin-Rastl, E.  
 Biochem. J. 251, 31-39, 1988  
 A>Title: Enolase isoenzymes in adult and developing Xenopus laevis and characterization  
 A:Reference number: S00463; MUID:88268812; PMID:3390159  
 A:Accession: S00463  
 A:Molecule type: mRNA  
 A:Residues: 1-434 <SRG>  
 A:Cross-references: UNIPROT:P08734; UNIPARC:UPI0000171530; EMBL:Y00718; NID:G64679; PI  
 C:Genetics:  
 A:Gene: ENO1  
 C:Function:  
 A:Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to ph  
 A:Pathway: gluconeogenesis; glycolysis  
 C:Superfamily: enolase  
 C:Keywords: carbon-oxygen lyase; dimer; gluconeogenesis; glycolysis; hydro-lyase; magn  
 F:40/Binding site: magnesium 2 (Ser) #status predicted  
 F:210,343/Active site: Glu, Lys #status predicted  
 F:245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 72.2%; Score 65; DB 1; Length 434;  
 Best Local Similarity 81.2%; Pred. No. 0.014;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTQIKTGAPC 16  
 DB 384 LVVGLCTQIKTGAPC 399

RESULT 7  
 JCI1039  
 phosphopyruvate hydratase (EC 4.2.1.11) - rat  
 N:Alternate names: neuron-specific enolase  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 05-Mar-1993 #sequence revision 19-Oct-1995 #text\_change 03-May-1996  
 C:Accession: JCI1039  
 R:Zhao, C.; Wang, L.B.; Song, X.W.; Zhang, J.Y.  
 Chinese Biochem. J. 10, 270-273, 1994  
 A>Title: cDNA cloning and sequencing of the NSE gene from rat brain.  
 A:Reference number: JCI1039  
 A:Accession: JCI1039  
 A:Molecule type: mRNA  
 A:Residues: 1-434 <ZHA>

A/Cross-references: UNIPARC:UPI000017606E  
A/Experimental source: brain, Miscar  
C/Comment: This enzyme is a specific marker protein for the development of nervous system  
A/Genes: nse  
C/Superfamily: enolase  
C/Keywords: brain; carbon-oxygen lyase; hydro-lyase

Query Match 72.2%; Score 65; DB 2; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.014;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 384 LVVGLCTGQIKTGAPC 399

## RESULT 8

JC4186  
phosphopyruvate hydratase (EC 4.2.1.11) alpha chain - chicken  
N/Alternate names: alpha-2-phospho-D-glycerate hydrolase; enolase  
C/Species: Gallus gallus (chicken)  
C/Date: 10-Sep-1995 #sequence\_revision 27-Oct-1995 #text\_change 09-Jul-2004  
C/Accession: JC4186

R/Tanaka, M.; Maeda, K.; Nakashima, K.  
J. Biochem. 117, 554-559, 1995  
A/Title: Chicken alpha-enolase but not beta-enolase has a Src-dependent tyrosine-phosphatase  
A/Reference number: JC4186; PMID:95355305; PMID:7629021

A/Accession: JC4186  
A/Molecule type: mRNA  
A/Residues: 1-434 <TRAN>

A/Cross-references: UNIPROT:P51913; UNIPARC:UPI0000171311; DDBJ:D37900; NID:G974175; PIR  
A/Experimental source: brain

C/Comment: This is a glycolytic enzyme and multiple isoenzyme forms were reported which  
rates for tyrosine phosphorylation in Rous sarcoma virus and is important in all the emb

C/Superfamily: enolase  
C/Keywords: carbon-oxygen lyase; hydro-lyase; phosphoprotein  
F/44/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 72.2%; Score 65; DB 2; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.014;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 384 LVVGLCTGQIKTGAPC 399

## RESULT 9

JC4187  
phosphopyruvate hydratase (EC 4.2.1.11) beta chain - chicken  
N/Alternate names: beta-2-phospho-D-glycerate hydrolase; enolase  
C/Species: Gallus gallus (chicken)  
C/Date: 14-Sep-1995 #sequence\_revision 27-Oct-1995 #text\_change 09-Jul-2004  
C/Accession: JC4187

R/Tanaka, M.; Maeda, K.; Nakashima, K.  
J. Biochem. 117, 554-559, 1995  
A/Title: Chicken alpha-enolase but not beta-enolase has a Src-dependent tyrosine-phosphatase  
A/Reference number: JC4186; PMID:95355305; PMID:7629021

A/Accession: JC4187  
A/Molecule type: mRNA  
A/Residues: 1-434 <TRAN>

A/Cross-references: UNIPROT:P07322; UNIPARC:UPI0000171312; DDBJ:D37901; NID:G974177; PIR  
C/Comment: This is a glycolytic enzyme and multiple isoenzyme forms were reported which  
rates for tyrosine phosphorylation in Rous sarcoma virus and is important in all the emb

C/Superfamily: enolase  
C/Keywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase; phosphoprotein  
F/1/Modified site: acetylated amino end (Met) #status experimental

Query Match 72.2%; Score 65; DB 2; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.014;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 384 LVVGLCTGQIKTGAPC 399

## RESULT 10

S06756  
phosphopyruvate hydratase (EC 4.2.1.11) beta - human  
N/Alternate names: enolase beta; enolase, skeletal muscle; phosphopyruvate hydratase, m  
C/Species: Homo sapiens (man)  
C/Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 09-Jul-2004  
C/Accession: S06756; S14759; S15933; S33330; S08685; S31650

R/Peshavaria, M.; Hinks, L.J.; Day, I.N.M.  
Nucleic Acids Res. 17, 8662, 1989  
A/Title: Structure of human muscle (beta) enolase mRNA and protein deduced from a genom  
A/Reference number: S06756; PMID:90067857; PMID:2587223

A/Accession: S06756  
A/Molecule type: mRNA  
A/Residues: 1-434 <PRS>

A/Cross-references: UNIPROT:P13929; UNIPARC:UPI00016A896; EMBL:X16504; NID:G31169; PIR  
R/Peshavaria, M.; Day, I.N.M.  
Biochem. J. 275, 427-433, 1991

A/Title: Molecular structure of the human muscle-specific enolase gene (ENO3).  
A/Reference number: S14759; PMID:91222137; PMID:1840492  
A/Accession: S14759

A/Status: nucleic acid sequence not shown  
A/Molecule type: DNA  
A/Residues: 1-434 <PE2>

A/Cross-references: UNIPARC:UPI00016A896; EMBL:X55976  
R/Call, L.; Peo, S.; Oliva, D.; Giallongo, A.  
Nucleic Acids Res. 18, 1893, 1990

A/Title: Nucleotide sequence of a cDNA encoding the human muscle-specific enolase (MSE)  
A/Reference number: S15933; PMID:90245587; PMID:2336366  
A/Accession: S15933

A/Molecule type: mRNA  
A/Residues: 1-84, 'A', '86-161, 'K', '163-434 <CAL>  
A/Cross-references: UNIPARC:UPI0000161C26; EMBL:X51957; NID:G34788; PIR:CAA36216.1; PIR

R/Giallongo, A.; Venturilla, S.; Oliva, D.; Barbieri, G.; Rubino, P.; Peo, S.  
Eur. J. Biochem. 214, 367-374, 1993  
A/Title: Structural features of the human gene for muscle-specific enolase. Differential

A/Reference number: S33330; PMID:93292497; PMID:8513787  
A/Accession: S33330  
A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA  
A/Residues: 1-161, 'K', '163-434 <GIA>  
A/Cross-references: UNIPARC:UPI000016A894; EMBL:X56832; NID:G31166; PIR:CAA40163.1; PIR

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1990  
A/Genetics: GDB:EN03  
A/Cross-references: GDB:119873; OMIM:131370

A/Map position: 17pter-17p12  
A/Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2  
C/Superfamily: enolase  
C/Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; muscle; skel

Query Match 72.2%; Score 65; DB 2; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.014;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 384 LVVGLCTGQIKTGAPC 399

RESULT 11  
S10246  
phosphopyruvate hydratase (EC 4.2.1.11) alpha - mouse  
N/Alternate names: 2-phosphoglycerate dehydratase; enolase alpha  
C/Species: Mus musculus (house mouse)  
C/Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 09-Jul-2004  
C/Accession: S10246; A56781

R/Kaghad, M.; Dumont, X.; Chalon, P.; Lelias, J.M.; Lamande, N.; Lucas, M.; Lazar, M.; C  
Nucleic Acids Res. 18, 3638, 1990

A>Title: Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from mouse brain.  
A/Reference number: S10246; MUID:90301487; PMID:2362815  
A/Accession: S10246  
A/Molecule type: mRNA  
A/Residues: 1-434 <KAG>  
A/Cross-references: UNIPROT:P17182, UNIPARC:UPI0000161F48; EMBL:X52379; NID:G55490; PIDN  
R:Botalicco, L.A.; Kendrick, N.C.; Keller, A.; Li, Y.; Tabas, I.  
A/Title: Cholesteryl ester loading of mouse peritoneal macrophages is associated with ch  
siform.  
A/Reference number: A56781; MUID:93152553; PMID:8427861  
A/Accession: A56781  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 'X', 60, 'X', 62-67, 'X', 69-71, 'XX', 100-109, 'X', 111-112, 'X', 114, 'X', 184-185, 'X',  
A/Cross-references: UNIPARC:UPI0000176064, UNIPARC:UPI0000176065; UNIPARC:UPI0000176066;  
A/Experimental source: peritoneal macrophages  
A/Note: sequence modified after extraction from NCBI backbone  
C/Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase  
Query Match 72.2%; Score 65; DB 2; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.014;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Oy 1 LVGLCTGQIKTGAPC 16  
Db 384 LVGLCTGQIKTGAPC 399  
RESULT 12  
S10247  
phosphorylase hydratase (EC 4.2.1.11) gamma - mouse  
C/Alternate names: 2-phosphoglycerate dehydratase; enolase gamma  
C/Species: Mus musculus (house mouse)  
C/Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 09-Jul-2004  
C/Accession: S10247  
R:Kashad, M.; Dumont, X.; Chalton, P.; Lelias, J.M.; Lemande, N.; Lucas, M.; Lazar, M.; C  
Nucleic Acids Res. 18, 3638, 1990  
A/Title: Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from mouse brain.  
A/Reference number: S10246; MUID:90301487; PMID:2362815  
A/Accession: S10247  
A/Molecule type: mRNA  
A/Residues: 1-434 <KAG>  
A/Cross-references: UNIPROT:P17183; UNIPARC:UPI0000001520; EMBL:X52380; NID:G55494; PIDN  
C/Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase  
Query Match 72.2%; Score 65; DB 2; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.014;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Oy 1 LVGLCTGQIKTGAPC 16  
Db 384 LVGLCTGQIKTGAPC 399  
RESULT 13  
S02072  
phosphorylase hydratase (EC 4.2.1.11) beta - rat  
C/Alternate names: enolase beta; enolase, muscle-specific  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 09-Jul-2004  
C/Accession: S02072  
R:Onahima, Y.; Mitsu, H.; Takayama, Y.; Kushiya, E.; Sakimura, K.; Takahashi, Y.  
FEBS Lett. 242, 425-430, 1989  
A/Title: cDNA cloning and nucleotide sequence of rat muscle-specific enolase (beta-beta  
A/Reference number: S02072; MUID:89121113; PMID:2914621  
A/Accession: S02072  
A/Molecule type: mRNA  
A/Residues: 1-434 <OHS>  
A/Cross-references: UNIPROT:P15429; UNIPARC:UPI0000167947; EMBL:X00979; NID:G57781; PIDN  
A/Note: the sequence from Fig. 4 is inconsistent with that from Fig. 2 in having 40-Asp

C/Superfamily: enolase  
C/Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; muscle  
Query Match 72.2%; Score 65; DB 2; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.014;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Oy 1 LVGLCTGQIKTGAPC 16  
Db 384 LVGLCTGQIKTGAPC 399  
RESULT 14  
A29170  
phosphorylase hydratase (EC 4.2.1.11) alpha - human  
C/Alternate names: 2-phosphoglycerate dehydratase; enolase 1; enolase alpha  
C/Species: Homo sapiens (man)  
C/Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 05-Oct-2004  
C/Accession: S11696; A29170; S52858; A39183  
R:Giallongo, A.; Olive, D.; Cali, L.; Barba, G.; Barbieri, G.; Feo, S.  
Eur. J. Biochem. 190, 567-573, 1990  
A/Title: Structure of the human gene for alpha-enolase.  
A/Reference number: S11696; MUID:90323004; PMID:2373081  
A/Accession: S11696  
A/Status: nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-434 <GTA>  
A/Cross-references: UNIPROT:P06733; UNIPARC:UPI000013C9AF; EMBL:X16288; NID:G31172; PI  
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1989  
R:Giallongo, A.; Feo, S.; Moore, R.; Croce, C.M.; Showe, L.C.  
Proc. Natl. Acad. Sci. U.S.A. 83, 6741-6745, 1986  
A/Title: Molecular cloning and nucleotide sequence of a full-length cDNA for human alpi  
A/Reference number: A29170; MUID:86313654; PMID:3529090  
A/Accession: A29170  
A/Molecule type: mRNA  
A/Residues: 1-434 <G12>  
A/Cross-references: UNIPARC:UPI000013C9AF; GB:M14328; NID:G182113; PIDN:AA52387.1; PI  
A/Note: the authors translated the codon AAG for residue 193 as His  
R:Walter, M.; Leidenberger, F.A.; Schwepp, K.W.; Berg, H.; Northemann, W.  
Submitted to the EMBL Data Library, February 1995  
A/Description: Autoreactive epitopes within the human alpha-enolase and their recogniti  
A/Reference number: S52858  
A/Accession: S52858  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-551, 'S', 253-434 <WAL>  
A/Cross-references: UNIPARC:UPI000016A207; EMBL:X84907; NID:G693932; PIDN:CAAS9331.1; F  
A/Experimental source: endometrium carcinoma cell line HEC-1B  
R:Miles, L.A.; Dahlberg, C.M.; Plestia, J.; Felez, J.; Kato, K.; Plow, E.F.  
Biochemistry 30, 1682-1691, 1991  
A/Title: Role of cell-surface lysines in plasminogen binding to cells: identification c  
A/Reference number: A39183; MUID:91129243; PMID:1847072  
A/Accession: A39183  
A/Molecule type: protein  
A/Residues: 170-182, 'I', 184, 'R', 186-190, 245-252 <MT>  
A/Cross-references: UNIPARC:UPI0000176068; UNIPARC:UPI0000176069  
C/Genetics:  
A/Gene: GDB:EN01  
A/Cross-references: GDB:119871; OMIM:172430  
A/Map position: 1p36-1p36  
A/Intons: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2  
C/Function:  
A/Description: catalyzes the reversible hydration of phosphoenolpyruvate to 2-phosphogl  
C/Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesium  
F,2-434/Product: phosphorylase hydratase alpha #status predicted <MAT>  
Query Match 72.2%; Score 65; DB 2; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.014;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Oy 1 LVGLCTGQIKTGAPC 16

```
Db      384 LVVGLCTGQIKTGAPC 399

RESULT 15
A23132
phosphopyruvate hydratase (EC 4.2.1.11) alpha - duck
N/Alternate names: enolase alpha; tau-crystallin
C/Species: Anas platyrhynchos (domestic duck)
C/Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 05-Oct-2004
C/Accession: A23132
R/Miscow, G.J.; Lieberman, T.; Williams, L.A.; Stapel, S.O.; de Jong, W.W.; Horwitz, J.; F
J. Cell Biol. 107, 2729-2736, 1988
A/Title: Tau-crystallin/alpha-enolase: one gene encodes both an enzyme and a lens struct
A/Reference number: A23750; MUID:89079778; PMID:2462567
A/Accession: A23132
A/Molecule type: mRNA
A/Residues: 1-434 <MS>
A/Cross-references: UNIPROT:P19140; UNIPARC:UPI00001711A5; GB:X14195; NID:g62455; PIDN:C
C/Superfamily: enolase
C/Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match      72.2%  Score 65;  DB 2;  Length 434;
Best Local Similarity 81.2%  Pred. No. 0.014;
Matches 13;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

QY      1 LVVGLCTGQIKTGAPC 16
Db      384 LVVGLCTGQIKTGAPC 399

RESULT 16
A24742
phosphopyruvate hydratase (EC 4.2.1.11) gamma - rat
N/Alternate names: 2-phospho-glycerate dehydratase; enolase gamma; neuronal enolase
C/Species: Rattus norvegicus (Norway rat)
C/Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 05-Oct-2004
C/Accession: A24742; PQ0006
R/Sakimura, K.; Kushiya, E.; Obinata, M.; Odani, S.; Takahashi, Y.
Proc. Natl. Acad. Sci. U.S.A. 82, 7453-7457, 1985
A/Title: Molecular cloning and the nucleotide sequence of cDNA for neuron-specific enola
A/Reference number: A24742; MUID:86042683; PMID:2865729
A/Accession: A24742
A/Molecule type: mRNA
A/Residues: 1-434 <SAK>
A/Cross-references: UNIPROT:P07323; UNIPARC:UPI00001694CA; GB:M11931; NID:g204041; PIDN:
R/Sakimura, K.; Kushiya, E.; Takahashi, Y.; Suzuki, Y.
Gene 60, 103-113, 1987
A/Title: The structure and expression of neuron-specific enolase gene.
A/Reference number: PQ0006; MUID:88152493; PMID:2450052
A/Accession: PQ0006
A/Molecule type: DNA
A/Residues: 1-28 <SA2>
A/Cross-references: UNIPARC:UPI000014B62B; GB:M22770; GB:M18742; NID:g205766; PIDN:AAA41
C/Superfamily: enolase
C/Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match      72.2%  Score 65;  DB 2;  Length 434;
Best Local Similarity 81.2%  Pred. No. 0.014;
Matches 13;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

QY      1 LVVGLCTGQIKTGAPC 16
Db      384 LVVGLCTGQIKTGAPC 399

RESULT 17
A23126
phosphopyruvate hydratase (EC 4.2.1.11) alpha - rat
N/Alternate names: enolase alpha; nonneuronal enolase
C/Species: Rattus norvegicus (Norway rat)
C/Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 05-Oct-2004
C/Accession: A23126
R/Sakimura, K.; Kushiya, E.; Obinata, M.; Takahashi, Y.

Nucleic Acids Res. 13, 4365-4378, 1985
A/Title: Molecular cloning and the nucleotide sequence of cDNA to mRNA for non-neuronal
A/Reference number: A23126; MUID:85242108; PMID:289793
A/Accession: A23126
A/Molecule type: mRNA
A/Residues: 1-434 <SAK>
A/Cross-references: UNIPROT:P04764; UNIPARC:UPI000015C86D; GB:X02610; NID:g56106; PIDN
C/Superfamily: enolase
C/Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match      72.2%  Score 65;  DB 2;  Length 434;
Best Local Similarity 81.2%  Pred. No. 0.014;
Matches 13;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

QY      1 LVVGLCTGQIKTGAPC 16
Db      384 LVVGLCTGQIKTGAPC 399

RESULT 18
T25040
hypothetical protein T21B10.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T25040
R/Baynes, C.
Submitted to the EMBL Data Library, December 1995
A/Reference number: Z19973
A/Accession: T25040
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-434 <Ntl>
A/Cross-references: UNIPROT:Q27527; UNIPARC:UPI0000164061; EMBL:Z68318; PIDN:CAA92692.1
A/Experimental source: clone T21B10
C/Genetics:
A/Gene: CESP:T21B10.2
A/Map position: 2
A/Intons: 29/1; 344/3
C/Superfamily: enolase

Query Match      62.2%  Score 56;  DB 2;  Length 434;
Best Local Similarity 75.0%  Pred. No. 0.35;
Matches 12;  Conservative 0;  Mismatches 4;  Indels 0;  Gaps 0;

QY      1 LVVGLCTGQIKTGAPC 16
Db      385 LVVGLATGQIKTGAPC 400

RESULT 19
S07586
phosphopyruvate hydratase (EC 4.2.1.11) - fruit fly (Drosophila melanogaster)
N/Alternate names: enolase
C/Species: Drosophila melanogaster
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C/Accession: S07586
R/Bishop, J.G.; Corces, V.G.
Nucleic Acids Res. 18, 191, 1990
A/Title: The nucleotide sequence of a Drosophila melanogaster enolase gene.
A/Reference number: S07586; MUID:90174924; PMID:2106662
A/Accession: S07586
A/Molecule type: DNA
A/Residues: 1-433 <Bis>
A/Cross-references: UNIPROT:P15007; UNIPARC:UPI0000129F6C; EMBL:X17034; NID:g7945; PIDN
C/Genetics:
A/Gene: FlyBase:Eno
A/Cross-references: FlyBase:FBgn0000579
A/Map position: 22A
C/Superfamily: enolase
C/Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match      61.1%  Score 55;  DB 2;  Length 433;
Best Local Similarity 75.0%  Pred. No. 0.49;
```

Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 LVGLCTCQIKTGAPC 16  
 |||||  
 Db 385 LVGLSTGQIKTGAPC 400

## RESULT 20

A3850  
 phosphopyruvate hydratase (EC 4.2.1.11), skeletal muscle - chicken  
 N/Alternate names: enolase, skeletal muscle  
 C/Species: Gallus gallus (chicken)  
 C/Date: 22-Jul-1987 #sequence\_revision 22-Jul-1987 #text\_change 05-Oct-2004  
 C/Accession: A23850; A60809  
 R/Russell, G.A.; Dunbar, B.; Fochergill-Gilmore, L.A.  
 Biochem. J. 236, 115-126, 1986  
 A/Title: The complete amino acid sequence of chicken skeletal-muscle enolase.  
 A/Reference number: A23850; MUID:87075592; PMID:3539098  
 A/Accession: A23850  
 A/Molecule type: protein  
 A/Residues: 1-433 <RUS>  
 A/Cross-references: UNIPROT:P07322; UNIPARC:UPI0000176060  
 R/Gibson, B.W.; Daley, D.J.; Williams, D.H.  
 Anal. Biochem. 169, 217-226, 1988  
 A/Title: Structural elucidation of N-terminal post-translational modifications by mass E

A/Reference number: A60809; MUID:88250539; PMID:2898218  
 A/Accession: A60809  
 A/Molecule type: protein  
 A/Residues: 1-9 <GIB>  
 A/Cross-references: UNIPARC:UPI0000176061  
 C/Comment: Several tissue-specific enolase isoenzymes are found in vertebrates.  
 C/Superfamily: enolase  
 C/Keywords: acetylated amino end; carbon-oxygen lyase; gluconeogenesis; glycolysis; hydr  
 F/1/Modified site: acetylated amino end (Ser) #status experimental  
 F/39/Binding site: magnesium 2 (Ser) #status predicted  
 F/209/Active site: Glu #status predicted  
 F/244,292,317/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 61.1%; Score 55; DB 2; Length 433;  
 Best Local Similarity 68.8%; Pred. No. 0.49;  
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 LVGLCTCQIKTGAPC 16  
 |||||  
 Db 383 LVGLCTCQIKTGAPC 398

## RESULT 21

A53665  
 phosphopyruvate hydratase (EC 4.2.1.11) - liver fluke  
 C/Species: Fasciola hepatica (liver fluke)  
 C/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 05-Oct-2004  
 C/Accession: A53665  
 J/Davies, R.E.; Singh, H.; Bocka, C.; Hardwick, C.; Ashraf el Mennawy, M.; Villanueva, J.  
 J. Biol. Chem. 269, 20026-20030, 1994  
 A/Title: RNA trans-splicing in Fasciola hepatica. Identification of a spliced leader (SL  
 A/Reference number: A53665; MUID:94327554; PMID:8051087  
 A/Accession: A53665  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-431 <DAV>  
 A/Cross-references: UNIPARC:UPI0000176070; GB:U10297; NID:9499266; PIDN:AAA57450.1; PID:  
 C/Superfamily: enolase  
 C/Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 58.9%; Score 53; DB 2; Length 431;  
 Best Local Similarity 75.0%; Pred. No. 1;  
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 LVGLCTCQIKTGAPC 16  
 |||||  
 Db 384 LVGLRTGQIKTGAPC 399

## RESULT 22

T03267  
 probable phosphopyruvate hydratase (EC 4.2.1.11) - rice  
 N/Alternate names: 2-phospho-D-glycerate hydrolase; enolase  
 C/Species: Oryza sativa (rice)  
 C/Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 09-Jul-2004  
 C/Accession: T03267  
 R/Hsing, Y.C.  
 submitted to the EMBL Data Library, May 1994  
 A/Reference number: Z14869  
 A/Accession: T03267  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Residues: 1-446 <HSI>  
 A/Cross-references: UNIPROT:Q42971; UNIPARC:UPI0000129F87; EMBL:U09450; NID:9780371; P  
 A/Experimental source: strain Tainung 67  
 C/Function:  
 A/Description: catalyzes the conversion of 2-phosphoglycerate to phosphoenolpyruvate  
 C/Superfamily: enolase  
 C/Keywords: carbon-oxygen lyase; glycolysis; hydro-lyase

Query Match 57.8%; Score 52; DB 2; Length 446;  
 Best Local Similarity 68.8%; Pred. No. 1.5;  
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 LVGLCTCQIKTGAPC 16  
 |||||  
 Db 395 LVGLATGQIKTGAPC 410

## RESULT 23

J01186  
 phosphopyruvate hydratase (EC 4.2.1.11) - tomato (fragment)  
 N/Alternate names: enolase  
 C/Species: Lycopersicon esculentum (tomato)  
 C/Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
 C/Accession: J01186  
 R/Van Der Straeten, D.; Rodrigues-Pousada, R.A.; Goodman, H.M.; Van Montagu, M.  
 Plant Cell 3, 719-735, 1991  
 A/Title: Plant enolase: gene structure, expression, and evolution.  
 A/Reference number: J01185; MUID:93044507; PMID:1841726  
 A/Accession: J01186  
 A/Molecule type: DNA  
 A/Residues: 1-326 <VAN>  
 A/Cross-references: UNIPROT:Q42887; UNIPARC:UPI00009E691; EMBL:X58109; NID:919205; PID  
 C/Comment: This enzyme is a ubiquitous enzyme that catalyzes the conversion of 2-phosph  
 C/Genetics:  
 A/Introns: 27/3; 61/3; 88/3; 113/3; 134/3; 160/3; 225/3; 242/3; 272/2; 289/3; 308/3  
 C/Superfamily: enolase  
 C/Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 56.7%; Score 51; DB 2; Length 326;  
 Best Local Similarity 68.8%; Pred. No. 1.6;  
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 LVGLCTCQIKTGAPC 16  
 |||||  
 Db 283 LVGLSTGQIKTGAPC 298

## RESULT 24

J01185  
 phosphopyruvate hydratase (EC 4.2.1.11) - tomato  
 N/Alternate names: enolase  
 C/Species: Lycopersicon esculentum (tomato)  
 C/Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
 C/Accession: J01185; S18191  
 R/Van Der Straeten, D.; Rodrigues-Pousada, R.A.; Goodman, H.M.; Van Montagu, M.  
 Plant Cell 3, 719-735, 1991  
 A/Title: Plant enolase: gene structure, expression, and evolution.  
 A/Reference number: J01185; MUID:93044507; PMID:1841726



```

A:Accession: J01185
A:Molecule type: mRNA
A:Residues: 1-444 <VAN>
A:Cross-references: UNIPROT:P26300; UNIPARC:UPI0000129F6; EMBL:X58108; NID:g19280; PIRN
A:Experimental source: cv. Orlando
A:Note: Introns in the coding regions for residues 1-110 and 437-444 are not revealed
C:Comment: This enzyme is a ubiquitous enzyme that catalyzes the conversion of 2-phospho
C:Gene:
A:Introns: 110/3; 137/3; 171/3; 198/3; 223/3; 244/3; 270/3; 335/3; 352/3; 382/2; 399/3;
C:Superfamily: enolase
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match          56.7%; Score 51; DB 2; Length 444;
Best Local Similarity 68.8%; Pred. No. 2.1;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGAPC 16
DB 393 LAVGLSTGQIKTGAPC 408

RESULT 25
J01187
phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana
N:Alternate names: enolase
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: J01187; F84781
R:Van Der Straeten, D.; Rodriguez-Ponsada, R.A.; Goodman, H.M.; Van Montagu, M.
Plant Cell 3, 719-735, 1991
A>Title: Plant enolase: gene structure, expression, and evolution.
A:Reference number: J01185; MUID:93044507; PMID:1841726
A:Accession: J01187
A:Molecule type: DNA
A:Residues: 1-444 <VAN>
A:Cross-references: UNIPROT:P25696; UNIPARC:UPI0000000D31; EMBL:X58107; NID:g16270; PIRN
M.; R. Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: F84781
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-444 <STO>
A:Cross-references: UNIPARC:UPI0000000D31; GB:AE002093; NID:g458151; PIRN:AA024635.1; C
C:Comment: This enzyme is a ubiquitous enzyme that catalyzes the conversion of 2-phospho
A:Gene: At2g36530
A:Map position: 2
A:Introns: 22/3; 65/3; 81/3; 110/3; 137/3; 198/3; 244/3; 270/3; 335/3; 399/3; 418/3
C:Superfamily: enolase
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match          56.7%; Score 51; DB 2; Length 444;
Best Local Similarity 68.8%; Pred. No. 2.1;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGAPC 16
DB 393 LAVGLSTGQIKTGAPC 408

RESULT 26
T02221
phosphopyruvate hydratase (EC 4.2.1.11) - maize
N:Alternate names: enolase
C:Species: Zea mays (maize)
C>Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C:Accession: T02221
R:Pal, S.K.; Lee, C.; Sachs, M.M.
Plant Physiol. 118, 1285-1293, 1998

```

```

A>Title: Differential regulation of enolase during anaerobiosis in maize.
A:Accession: Z14628; MUID:99063764; PMID:9847102
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-446 <LAL>
A:Cross-references: UNIPROT:P42895; UNIPARC:UPI0000129F41; EMBL:U17973; NID:g602252; PIR
A:Experimental source: strain B73Ht; roots
C:Gene: eno2
C:Function:
A:Description: catalyzes the reversible dehydration of 2-phospho-D-glycerate to phospho
C:Superfamily: enolase
C:Keywords: carbon-oxygen lyase; hydro-lyase; magnesium
F:43/Binding site: magnesium 2 (ser) #status predicted
F:216/354/Active site: Glu, Lys #status predicted
F:251/302/329/Binding site: magnesium 1 (asp, Glu, Asp) #status predicted

Query Match          56.7%; Score 51; DB 2; Length 446;
Best Local Similarity 68.8%; Pred. No. 2.1;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGAPC 16
DB 395 LAVGLSTGQIKTGAPC 410

RESULT 27
S39203
phosphopyruvate hydratase (EC 4.2.1.11) - caenor bean
N:Alternate names: enolase
C:Species: Ricinus communis (castor bean)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S39203
R:Blakeley, S.D.; Cole, K.C.; Dennis, D.T.
submitted to the EMBL Data Library, November 1993
A:Description: Isolation of a full length cDNA clone encoding cytosolic enolase from Ri
A:Reference number: S39203
A:Accession: S39203
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-445 <BLA>
A:Cross-references: UNIPROT:P42896; UNIPARC:UPI0000129F92; EMBL:Z28386; NID:g433608; PIR
C:Superfamily: enolase
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match          55.6%; Score 50; DB 2; Length 445;
Best Local Similarity 68.8%; Pred. No. 3;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGAPC 16
DB 394 LSVGLATGQIKTGAPC 409

RESULT 28
T12341
phosphopyruvate hydratase (EC 4.2.1.11) - common ice plant
N:Alternate names: 2-phospho-D-glycerate hydratase; enolase
C:Species: Mesembryanthemum crystallinum (common ice plant)
C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C:Accession: T12341
R:Forsthoefel, N.R.; Cushman, M.F.; Cushman, J.C.
submitted to the EMBL Data Library, April 1994
A:Description: Characterization and stress-induced expression of enolase from the facult
A:Reference number: Z17497
A:Accession: T12341
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-444 <FOR>
A:Cross-references: UNIPROT:Q43130; UNIPARC:UPI000016DE3B; EMBL:U09194; NID:g533473; PIR
C:Function:

```



A:Description: catalyzes the conversion of 2-phosphoglycerate to phosphoenolpyruvate  
 C:Superfamily: enolase  
 C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 54.4%; Score 49; DB 2; Length 444;  
 Best Local Similarity 68.8%; Pred. No. 4.3;  
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVVGLCTQIKTGAPC 16  
 DB 393 LSVGLSTGQIKTGAPC 408

## RESULT 29

S16257  
 phosphopyruvate hydratase (EC 4.2.1.11) - maize  
 N:Alternate names: enolase  
 C:Species: Zea mays (maize)  
 C>Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
 C:Accession: S16257  
 R:Lal, S.K.; Johnson, S.; Conway, T.; Kelley, P.M.  
 Plant Mol. Biol. 16, 787-795, 1991  
 A>Title: Characterization of a maize cDNA that complements an enolase-deficient mutant C  
 A:Reference number: S16257; MUID:91316216; PMID:1859865  
 A:Accession: S16257  
 A:Molecule type: mRNA  
 A:Residues: 1-446 <LAL>  
 A:Cross-references: UNIPROT:P26301; UNIPARC:UPI0000129F3D; EMBL:X55981; NID:g22272; PIDN  
 C:Superfamily: enolase  
 C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match 54.4%; Score 49; DB 2; Length 446;  
 Best Local Similarity 68.8%; Pred. No. 4.3;  
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVVGLCTQIKTGAPC 16  
 DB 395 LSVGLSTGQIKTGAPC 410

## RESULT 30

S24996  
 phosphopyruvate hydratase (EC 4.2.1.11) - Chlamydomonas reinhardtii  
 N:Alternate names: enolase  
 C:Species: Chlamydomonas reinhardtii  
 C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
 C:Accession: S24996  
 R:Dumont, F.  
 submitted to the EMBL Data Library, May 1992  
 A:Reference number: S24989  
 A:Accession: S24996  
 A:Molecule type: mRNA  
 A:Residues: 1-372 <DUM>  
 A:Cross-references: UNIPROT:P31683; UNIPARC:UPI0000129F64; EMBL:X66412; NID:gl8142; PIDN  
 C:Superfamily: enolase  
 C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 53.3%; Score 48; DB 2; Length 372;  
 Best Local Similarity 62.5%; Pred. No. 5.3;  
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVVGLCTQIKTGAPC 16  
 DB 323 LAVGLASGQIKTGAPC 338

Search completed: April 3, 2006, 08:04:35  
 Job time : 17 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 08:02:35 ; Search time 56 Seconds  
(without alignments)  
201.580 Million cell updates/sec

Title: US-09-647-457F-3  
Perfect score: 90  
Sequence: 1 LVGLCTCQIKTGPAC 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_crembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	82.2	458	1	ENO1B_HUMAN
2	68	72.2	433	1	ENO1B_BOVIN
3	65	72.2	88	2	Q80416_ICTPU
4	65	72.2	154	2	Q9NPL4_HUMAN
5	65	72.2	159	2	Q9NG70_9BILA
6	65	72.2	184	2	Q96GV1_HUMAN
7	65	72.2	259	2	Q7Z2M5_SPAAU
8	65	72.2	272	2	Q9BT62_HUMAN
9	65	72.2	338	2	Q922A0_MOUSE
10	65	72.2	366	2	Q6PHC1_MOUSE
11	65	72.2	377	2	Q6LDC3_ANAPL
12	65	72.2	383	2	Q9NG67_9HEXA
13	65	72.2	394	2	Q9PTX6_LAMRE
14	65	72.2	395	1	ENO_ALIMI
15	65	72.2	395	2	Q9U5F7_EPTBU
16	65	72.2	395	2	Q9PTX5_LAMRE
17	65	72.2	406	2	Q4SZW2_TETNG
18	65	72.2	420	2	Q5ISQ0_MACFA
19	65	72.2	431	2	Q4TBD1_TETNG
20	65	72.2	432	2	Q6T0P5_BRARE
21	65	72.2	432	2	Q6FC12_BRARE
22	65	72.2	433	1	ENO_ALIMI
23	65	72.2	433	1	ENO_ANAPL
24	65	72.2	433	1	ENO_CHICK
25	65	72.2	433	1	ENO_HUMAN
26	65	72.2	433	1	ENO_MOUSE
27	65	72.2	433	1	ENO_PYTRG
28	65	72.2	433	1	ENO_RAT
29	65	72.2	433	1	ENO_SCEUN
30	65	72.2	433	1	ENO_TRASC
31	65	72.2	433	1	ENO_CHICK

32	65	72.2	433	1	ENO_HUMAN	P13929 homo sapien
33	65	72.2	433	1	ENO_MOUSE	P21550 mus musculu
34	65	72.2	433	1	ENO_RABIT	P25704 oryctolagus
35	65	72.2	433	1	ENO_RAT	P15429 rattus norv
36	65	72.2	433	1	ENO_HUMAN	P09104 homo sapien
37	65	72.2	433	1	ENO_MOUSE	P17183 mus musculu
38	65	72.2	433	1	ENO_RAT	P07323 rattus norv
39	65	72.2	433	1	ENO_HOMGA	P56552 homarus gam
40	65	72.2	433	1	ENO_MOUSE	P08734 xenopus lae
41	65	72.2	433	2	Q6FC89_BRARE	Q6FC89 brachydanio
42	65	72.2	433	2	Q6TH14_BRARE	Q6TH14 brachydanio
43	65	72.2	433	2	Q568G3_BRARE	Q568G3 brachydanio
44	65	72.2	434	1	ENO_LOLPE	Q02654 loligo peal
45	65	72.2	434	1	ENO_SCHMA	P33676 schistosoma
46	65	72.2	434	1	ENO_SCHMA	Q27877 schistosoma
47	65	72.2	434	2	Q6F5V6_HUMAN	Q6F5V6 homo sapien
48	65	72.2	434	2	Q4TUS4_HUMAN	Q4TUS4 homo sapien
49	65	72.2	434	2	Q53HR3_HUMAN	Q53HR3 homo sapien
50	65	72.2	434	2	Q53FT9_HUMAN	Q53FT9 homo sapien
51	65	72.2	434	2	Q96656_PENMO	Q96656 penaeus mon
52	65	72.2	434	2	Q5D135_SCHUA	Q5D135 schistosoma
53	65	72.2	434	2	Q5DDV5_SCHUA	Q5DDV5 schistosoma
54	65	72.2	434	2	Q5R6Y1_PONPY	Q5R6Y1 pongo pygma
55	65	72.2	434	2	Q4R5L2_MACFA	Q4R5L2 macaca fasc
56	65	72.2	434	2	Q5SXS8_MOUSE	Q5SXS8 mus musculu
57	65	72.2	434	2	Q5XIV3_RAT	Q5XIV3 rattus norv
58	65	72.2	434	2	Q545V3_MOUSE	Q545V3 mus musculu
59	65	72.2	434	2	Q5FW97_MOUSE	Q5FW97 mus musculu
60	65	72.2	434	2	Q4FKS5_MOUSE	Q4FKS5 mus musculu
61	65	72.2	434	2	Q8JF80_CROPL	Q8JF80 crocodylus
62	65	72.2	434	2	Q7ZXAX_XENIA	Q7ZXAX xenopus lae
63	65	72.2	434	2	Q8AVT0_XENIA	Q8AVT0 xenopus lae
64	65	72.2	434	2	Q6G0M9_BRARE	Q6G0M9 brachydanio
65	65	72.2	434	2	Q7S2Z5_XENIA	Q7S2Z5 xenopus lae
66	65	72.2	434	2	Q4VA70_XENTRA	Q4VA70 xenopus tro
67	65	72.2	434	2	Q4RXG6_TETNG	Q4RXG6 tetraodon n
68	65	72.2	436	2	Q5DCP8_SCHUA	Q5DCP8 schistosoma
69	65	72.2	458	2	Q5XKX1_MOUSE	Q5XKX1 mus musculu
70	65	72.2	462	2	Q5XUG8_MOUSE	Q5XUG8 mus musculu
71	65	72.2	463	2	Q4QRP1_RAT	Q4QRP1 rattus norv
72	65	72.2	464	2	Q5B9J3_RAT	Q5B9J3 rattus norv
73	65	72.2	464	2	Q5EB49_RAT	Q5EB49 rattus norv
74	61	67.8	387	2	Q5WQLO_PHATRA	Q5WQLO phaeodactyl
75	61	67.8	389	2	Q5WQW2_9STRA	Q5WQW2 heterosigma
76	61	67.8	430	2	Q5U0Y7_HETTR	Q5U0Y7 heterosigma
77	59	65.6	434	1	ENO_CHICK	Q5U971 limulus gall
78	58	64.4	251	2	Q9NG71_LIMPO	Q9NG71 limulus gall
79	56	62.2	337	2	Q814P9_CABEL	Q814P9 caenorhabdi
80	56	62.2	433	1	ENO_CABEL	Q27527 caenorhabdi
81	56	62.2	434	2	Q61Z94_CABER	Q61Z94 caenorhabdi
82	56	62.2	437	2	Q67U00_TRISP	Q67U00 trichinella
83	56	62.2	465	2	Q6A4N1_CABEL	Q6A4N1 caenorhabdi
84	55	61.1	159	2	Q9NG73_9HEXA	Q9NG73 eunesocampa
85	55	61.1	358	2	Q56RP1_DROAI	Q56RP1 dirosophila
86	55	61.1	371	2	Q967N8_9CUCU	Q967N8 hyocoryphal
87	55	61.1	373	2	Q56RN9_DROMI	Q56RN9 dirosophila
88	55	61.1	384	2	Q9NG68_9MYRI	Q9NG68 scolopendra
89	55	61.1	409	2	Q56RN2_DROMI	Q56RN2 dirosophila
90	55	61.1	409	2	Q56RN2_DROMI	Q56RN2 dirosophila
91	55	61.1	413	2	Q44100_DROPS	Q44100 dirosophila
92	55	61.1	413	2	Q44101_DROSU	Q44101 dirosophila
93	55	61.1	433	2	Q7Q3D8_ANOGA	Q7Q3D8 anopheles g
94	55	61.1	433	2	Q5XKS5_9HEMI	Q5XKS5 oncometopia
95	55	61.1	442	2	Q4N1N1_9HEPA	Q4N1N1 theileria p
96	55	61.1	442	2	Q4UBV7_9HEPA	Q4UBV7 theileria p
97	55	61.1	500	1	ENO_DROME	P15007 dirosophila
98	53	58.9	433	1	ENO_PASHE	Q27655 fasciola he
99	53	58.9	433	2	Q93873_PBECA	Q93873 pneumocysti
100	53	58.9	434	2	Q54RK5_DICDI	Q54RK5 dictyosteli

## ALIGNMENTS

```

RESULT 1
ENOB_HUMAN STANDARD; PRT; 458 AA.
ID ENOB_HUMAN STANDARD; PRT; 458 AA.
AC Q05524;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Alpha enolase, lung specific (EC 4.2.1.11) (2-phospho-D-glycerate
hydro-lyase) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase)
DE (HELI).
GN Name=ENO1B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung fibroblast;
RX MEDLINE=93372640; PubMed=7689884;
RA Verma M., Kuri R.N.;
RT "Human lung enolase: cloning and sequencing of cDNA and its
inducibility with dexamethasone."
RL Biochem. Mol. Biol. Int. 30:293-303 (1993).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
H(2)O.
CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing
the dimer.
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- INDUCTION: By dexamethasone.
CC -1- SIMILARITY: Belongs to the enolase family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL, X66610; CAA47179.1; -; mRNA.
DR PIR, I37360; I37360.
DR HSSP, P56252; 1PDZ.
DR Reactome; Q05524; -.
DR MIM, 607098; -.
DR GO; GO:0004634; F:phosphopyruvate hydratase activity; TAS.
DR InterPro; IPR000941; Enolase.
DR PANTHER; PTHR11902; Enolase; 1.
DR Pfam; PF00113; Enolase_C; 1.
DR Pfam; PF03952; Enolase_N; 1.
DR PRINTS; PR00148; ENOLASE.
DR PRODOM; PD000902; Enolase; 1.
DR TIGRFAIR; TIGR01060; eno; 1.
DR PROSITE; PS00164; ENOLASE; 1.
KW Glycolysis; Lyase; Magnesium; Metal-binding; Multigene family.
FT ACT SITE 167
FT METAL 254 254 By similarity.
FT METAL 308 308 Magnesium (By similarity).
FT METAL 336 336 Magnesium (By similarity).
FT METAL 336 336 Magnesium (By similarity).
SQ SEQUENCE 458 AA; 49477 MW; 2590F34A28F44314 CRC64;
Query Match 82.2%; Score 74; DB 1; Length 458;
Best Local Similarity 87.5%; Pred. No. 0.0017;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 LVVGLCTQIKTGPAC 16
Db 407 LVVGLCTQIKTGPAC 422

```

RESULT 2  
ENOB\_BOVIN

```

ID ENOB_BOVIN STANDARD; PRT; 433 AA.
AC Q9XSJ4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-
neural enolase) (NNE) (Enolase I) (Phosphopyruvate hydratase) (HAP47).
GN Name=ENO1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chapman K.T., Newman B., Hillyard M.C., Freemont A.J., Grant M.E.,
RA Boot-Handford R., Wallis G.A.;
RT "Alpha enolase is upregulated in proliferative chondrocytes in the
epiphyseal growth plate and in human osteoarthritic tissue."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP PROTEIN SEQUENCE OF 269-280 AND 372-393, AND FUNCTION AS AN
ENDOTHELIAL HYPOXIC STRESS PROTEIN.
RX MEDLINE=96070906; PubMed=7499243; DOI=10.1074/jbc.270.46.2752;
RA Aronson R.M., Graven K.K., Tucci M., McDonald R.J., Farber H.W.;
RT "Non-neuronal enolase is an endothelial hypoxic stress protein."
RL J. Biol. Chem. 270:2752-2757 (1995).
CC -1- FUNCTION: Multifunctional enzyme that, as well as its role in
glycolysis, plays a part in various processes such as growth
control, hypoxia tolerance and allergic responses. May also
function in the intravascular and pericellular fibrolytic system
due to its ability to serve as a receptor and activator of
plasminogen on the cell surface of several cell-types such as
leukocytes and neurons (By similarity).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
H(2)O.
CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing
the dimer (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Mammalian enolase is composed of 3 isozyme subunits,
alpha, beta and gamma, which can form homodimers or heterodimers
which are cell-type and development-specific. ENO1 interacts with
PLG in the neuronal plasma membrane and promotes its activation.
The C-terminal lysine is required for this binding (By
similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Can translocate to the plasma
membrane in either the homodimeric (alpha/alpha) or heterodimeric
(alpha/gamma) form (By similarity). ENO1 is localized to the M-
band (By similarity).
CC -1- TISSUE SPECIFICITY: The alpha/alpha homodimer is expressed in
embryo and in most adult tissues. The alpha/beta heterodimer and
the beta/beta homodimer are found in striated muscle, and the
alpha/gamma heterodimer and the gamma/gamma homodimer in neurons.
DEVELOPMENTAL STAGE: During ontogenesis, there is a transition
from the alpha/alpha homodimer to the alpha/beta heterodimer in
striated muscle cells, and to the alpha/gamma heterodimer in nerve
cells.
CC -1- INDUCTION: Expression increased up to 3-fold by hypoxic stress in
vascular endothelial cells.
CC -1- SIMILARITY: Belongs to the enolase family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL, AF149256; AAD33073.1; -; mRNA.
DR HSSP, Q9NDR8; 1OEP.
DR SMR; Q9XSJ4; 1-430.
DR InterPro; IPR000941; Enolase.
DR PANTHER; PTHR11902; Enolase; 1.
DR Pfam; PF00113; Enolase_C; 1.

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DR Pfam; PF03952; Enolase N; 1.
DR PRINTS; PR00148; ENOLASE.
DR ProDom; PD000902; Enolase; 1.
DR TIGRfam; TIGR01060; eno; 1.
DR PROSITE; PS00164; ENOLASE; 1.
KW Direct protein sequencing; Glycolysis; Lyase; Magnesium;
KW Metal-binding; Multigene family; Plasmidogen activation.
FT INIT MET 0
FT REGION 404 433 Required for interaction with PLG (By
FT similarity).
FT ACT SITE 157 157 By similarity.
FT METAL 244 244 Magnesium (By similarity).
FT METAL 292 292 Magnesium (By similarity).
FT METAL 317 317 Magnesium (By similarity).
SQ SEQUENCE 433 AA; 47146 MW; B004E965C46F2E0C CRC64;

Query Match 75.6%; Score 68; DB 1; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.015;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 LVVGLCTGQIKTGAPC 16
Db 383 LVVGLCTGQIKTGAPC 398

RESULT 3
0804Y6 ICTPU PRT; 88 AA.
ID 0804Y6 ICTPU PRELIMINARY;
AC 0804Y6;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Enolase (Fragment).
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxId=7998;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA TISSUE=Muscle;
RA Kim S., Li P., Zheng X., Dunham R.A., Liu Z.;
RT "Gene expression in the muscles of young and mature channel catfish
RT (Ictalurus punctatus) as analyzed by expressed sequence tags and gene
RT filters."
RL Fish Physiol. Biochem. 0:0-0(2003).
DR EMBL; AF227804; AA025761.1; -; mRNA.
DR HSSP; P56252; 1PDZ.
DR SMR; 0804Y6; 4-85.
DR GO; GO:0000015; C:phosphopyruvate hydratase complex; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR000941; Enolase.
DR Pfam; PF00113; Enolase C; 1.
DR ProDom; PD000902; Enolase; 1.
DR NON TER 1
SQ SEQUENCE 88 AA; 9830 MW; 8C14B5E5FDEB36C1 CRC64;

Query Match 72.2%; Score 65; DB 2; Length 88;
Best Local Similarity 81.2%; Pred. No. 0.011;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 LVVGLCTGQIKTGAPC 16
Db 38 LVVGLCTGQIKTGAPC 53

RESULT 4
09NPL4 HUMAN PRT; 154 AA.
ID 09NPL4 HUMAN PRELIMINARY;
AC 09NPL4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)

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DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Carnivora; Homnidae;
OC Homo.
OX NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Auffray C., Ansoyge W., Ballabio A., Estivill X., Gibson K.,
RA Lehrach H., Pouscka A., Lundberg J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Andreu N., Escivill X., Escarceller M., Suney L.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
CC H(2)O.
CC -1- COPFACTOR: Magnesium. Required for catalysis and for stabilizing
CC the dimer (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the enolase family.
DR EMBL; AL35213; CAB94588.1; -; mRNA.
DR HSSP; P56252; 1PDZ.
DR SMR; 09NPL4; 1-151.
DR Ensemble; ENSG00000108515; Homo sapiens.
DR GO; GO:0000015; C:phosphopyruvate hydratase complex; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR000941; Enolase.
DR Pfam; PF00113; Enolase C; 1.
DR PRINTS; PR00148; ENOLASE.
DR ProDom; PD000902; Enolase; 1.
DR PROSITE; PS00164; ENOLASE; 1.
KW Glycolysis; Lyase; Magnesium.
FT NON TER 1
SQ SEQUENCE 154 AA; 16939 MW; 347B95809B1C864D CRC64;

Query Match 72.2%; Score 65; DB 2; Length 154;
Best Local Similarity 81.2%; Pred. No. 0.019;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 LVVGLCTGQIKTGAPC 16
Db 104 LVVGLCTGQIKTGAPC 119

RESULT 5
09NG70 9BILA PRELIMINARY; PRT; 159 AA.
ID 09NG70 9BILA PRELIMINARY;
AC 09NG70;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Enolase (Fragment).
OS Peripatus sp. Per3.
OC Eukaryota; Metazoa; Onychophora; Peripatidae; Peripatus.
OX NCBI_TaxId=126380;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Regier J.C., Shultz J.W.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
CC H(2)O.
CC -1- COPFACTOR: Magnesium. Required for catalysis and for stabilizing
CC the dimer (By similarity).
CC -1- PATHWAY: Glycolysis.

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CC -1 SUBUNIT: Homodimer (By similarity).  
CC -1 SUBUNIT: Belongs to the enolase family.  
CC -1 SIMILARITY: Belongs to the enolase family.  
DR EMBL: AF258667; AAF2638.1; -; mRNA.  
DR HSPB; P56252; 1BD2.  
DR SNR; Q9NG70; 1-159.  
DR GO; GO:0000015; C:phosphopyruvate hydratase complex; IEA.  
DR GO; GO:0016829; F:lyase activity; IEA.  
DR GO; GO:0000287; F:magnesium ion binding; IEA.  
DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.  
DR GO; GO:0006096; P:glycolysis; IEA.  
DR InterPro; IPR000941; Enolase.  
DR Pfam; PF00113; Enolase\_C.1.  
DR PRINTS; PR00148; ENOLASE.  
DR PROSITE; PS00164; ENOLASE; 1.  
DR GlycoLyse; Lyase; Magnesium.  
FT NON\_TER 1  
FT TER 159  
SQ SEQUENCE 159 AA; 17583 MW; 840E266ACD936D3CD CRC64;  
  
Query Match 72.2%; Score 65; DB 2; Length 159;  
Best Local Similarity 81.2%; Pred. No. 0.019;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 LVVGLCTQIKTGAPC 16  
Db 138 LVVGLCTQIKTGAPC 153  
  
RESULT 6  
Q96GV1\_HUMAN  
ID Q96GV1\_HUMAN PRELIMINARY; PRT; 184 AA.  
AC Q96GV1;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE ENO1 protein (Fragment).  
GN Name:ENO1;  
GN Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Ovary;  
RX MEDLINE=22388257; PubMed=14277932; DOI=10.1073/pnas.242603899;  
RA Strengberg R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carantini P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnaracne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fanev J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Buterfield J.S.N., Krzywinski M.I., Skalek U., Smallus D.E.,  
RA Scherach A., Schein J.E., Jones S.J.M., Matra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Ovary;  
RA Strauberg R.;  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
CC -1 CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +

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CC CC H(2)O.
CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing
CC the dimer (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the enolase family.
CC EMBL: BC009218; AA09218.2; -; mRNA.
DR DR HSP, P56252; 1PZD.
DR SMR; Q96GV1; 1-181.
DR Ensemble1; ENSG00000074800; Homo sapiens.
DR GO; GO:0000015; C:phosphopyruvate hydratase complex; IEA.
DR GO; GO:0016629; F:lyase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.
DR InterPro; IPR000941; Enolase.
DR Pfam; PF00113; Enolase_C1.
DR PRINTS; PR00148; ENOLASE.
DR Prodom; PD000902; ENOLASE_C1.
DR PROSITE; PS00164; ENOLASE; 1.
FT Glycolysis; Lyase; Magnesium.
FT NON_TER 1 1
SQ SEQUENCE 184 AA; 20415 MW; F94E113824E5290A CRC64;

Query Match 72.2%; Score 65; DB 2; length 184;
Best Local Similarity 81.2%; Pred. No. 0.024;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0.

QY 1 LVGLCTGQIKTGPA 16
DB 134 LVGLCTGQIKTGAPC 149

RESULT 7
O7ZZM5_SPAU PRELIMINARY; PRT; 259 AA.
ID O7ZZM5;
AC O7ZZM5;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Enolase (Fragment).
OS Sparus aurata (Gilthead sea bream).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percormorpha; Perciformes; Percoidae;
OC Sparidae; Sparus.
OX NCBI_TaxID=8175;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain.
RA Ribes L., Planas J.V., Monetti C., Bernardini G., Saroglia M.,
RA Tort L., Mackenzie S.;
RT "A differentially expressed enolase gene isolated from the gilthead
RT sea bream (Sparus aurata) under high-density conditions is up-
RT regulated in brain after in vivo lipopolysaccharide challenge.";
RL Agaculture 241:195-206 (2004).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
CC H(2)O.
CC -1- PATHWAY: Glycolysis.
CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing
CC the dimer (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC EMBL; AY263379; AAC092646.1; -; mRNA.
DR HSSP; P56252; 1PZD.
DR SMR; O7ZZM5; 1D28.
DR GO; GO:0000015; C:phosphopyruvate hydratase complex; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.

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DR InterPro: IPR000941; Enolase.  
 DR Pfam: PF00113; Enolase C; 1.  
 DR PRINTS: PR00148; ENOLASE.  
 DR ProDom: PD000902; ENOLASE; 1.  
 DR PROSITE: PS00164; ENOLASE; 1.  
 DR GlycoLysis: Lyase; Magnesium.  
 FT NON TER 1 259  
 FT NON TER 1 259  
 SQ SEQUENCE 259 AA; 26484 MW; 1DE915D3B955311B CRC64;

Query Match 72.2%; Score 65; DB 2; Length 259;  
 Best Local Similarity 81.2%; Pred. No. 0.03;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTQIKTGAPC 16  
 Db 209 LVVGLCTQIKTGAPC 224

RESULT 8  
 Q9BT62 HUMAN PRELIMINARY; PRT; 272 AA.

ID Q9BT62; 01-JUN-2001 (TRENBLrel. 17, Created)  
 AC Q9BT62; 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE ENO1 protein (Fragment).  
 GN Name=ENO1;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Placenta;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shemen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheeler C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullish S.J.,  
 RA Bock S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Placenta;  
 RA Strausberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing  
 the dimer (By similarity).  
 CC -1- PATHWAY: Glycolysis.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUSCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: Belongs to the enolase family.  
 DR EMBL: BC004325; AA04325.1; -; mRNA.  
 DR HSRP; P56252; 1P2.  
 DR SMR; Q9BT62; 1-269.

DR Ensembl; ENSG00000074800; Homo sapiens.  
 DR GO; GO:0006015; C:phosphopyruvate hydratase complex; IEA.  
 DR GO; GO:0016829; P:lyase activity; IEA.  
 DR GO; GO:0000287; F:magnesium ion binding; IEA.  
 DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.  
 DR GO; GO:0006096; P:glycolysis; IEA.  
 DR InterPro: IPR000941; Enolase.  
 DR Pfam: PF00113; Enolase C; 1.  
 DR PRINTS: PR00148; ENOLASE.  
 DR ProDom: PD000902; ENOLASE; 1.  
 DR PROSITE: PS00164; ENOLASE; 1.  
 DR GlycoLysis: Lyase; Magnesium.  
 FT NON TER 1 272  
 FT NON TER 1 272  
 SQ SEQUENCE 272 AA; 29883 MW; 08F1755ADEA88DDC CRC64;

Query Match 72.2%; Score 65; DB 2; Length 272;  
 Best Local Similarity 81.2%; Pred. No. 0.03;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTQIKTGAPC 16  
 Db 222 LVVGLCTQIKTGAPC 237

RESULT 9  
 Q922A0 MOUSE PRELIMINARY; PRT; 338 AA.

ID Q922A0; 01-DEC-2001 (TRENBLrel. 19, Created)  
 AC Q922A0; 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Eno2 protein (Fragment).  
 GN Name=Eno2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shemen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheeler C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullish S.J.,  
 RA Bock S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
 RA Strausberg R.;  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing  
 the dimer (By similarity).  
 CC -1- PATHWAY: Glycolysis.  
 CC -1- SUBUNIT: Homodimer (By similarity).

```
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the enolase family.
DR EMBL: BC009018, AAH09018.1, -, mRNA.
DR HSSP: P56252, 1PD2.
DR SMR: Q922A0, 25-143, 125-338.
DR Ensembl: ENSMUSG0000004267, Mus musculus.
DR MGI: MGI:95394, Eno2.
DR GO: GO:0000015, C:phosphopyruvate hydratase complex, IEA.
DR GO: GO:0016829, P:lyase activity, IEA.
DR GO: GO:0000287, F:magnesium ion binding, IEA.
DR GO: GO:0004634, F:phosphopyruvate hydratase activity, IEA.
DR GO: GO:0006096, P:glycolysis, IEA.
DR InterPro: IPR000941, Enolase.
DR Pfam: PF00113, Enolase_C_1.
DR Pfam: PF03952, Enolase_N_1.
DR ProDom: PD000902, Enolase_1.
DR PROSITE: PS00164, ENOLASE, 1.
DR GlycoSite: Lysase, Magnesium.
FT NON_TER
SQ SEQUENCE 338 AA; 37146 MW; B0F2F321D7749484 CRC64;

Query Match 72.2%; Score 65; DB 2; Length 338;
Best Local Similarity 81.2%; Pred. No. 0.038;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
DB 288 LVVGLCTGQIKTGAPC 303

RESULT 10
06PHCL_MOUSE
ID 06PHCL_MOUSE PRELIMINARY; PRT; 366 AA.
AC 06PHCL;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Eno1 protein.
GN Eno1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toohyuki S., Carninci P., Mullen C.,
RA Bosak S.A., Loquellano N.A., Peters G.J., Abramson R.D., Millhys S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rahcy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maris M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.,
RT Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
```

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DR EMBL: BC056611, AAH56611.1, -, mRNA.
DR SMR: 06PHCL; 3-363.
DR MGI: MGI:95393, Eno1.
DR GO: GO:0005515, F:protein binding, TAS.
DR InterPro: IPR000941, Enolase.
DR Pfam: PF00113, Enolase_C_1.
DR Pfam: PF03952, Enolase_N_1.
DR PRINTS: PR00148, ENOLASE.
DR ProDom: PD000902, Enolase_1.
DR TIGRFAMs: TIGR01060, eno, 1.
DR PROSITE: PS00164, ENOLASE, 1.
SQ SEQUENCE 366 AA; 39782 MW; 11E90DDDE4B67D1 CRC64;

Query Match 72.2%; Score 65; DB 2; Length 366;
Best Local Similarity 81.2%; Pred. No. 0.04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
DB 316 LVVGLCTGQIKTGAPC 331

RESULT 11
06LDK3_ANAPL
ID 06LDK3_ANAPL PRELIMINARY; PRT; 377 AA.
AC 06LDK3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-enolase/tau-crystallin (EC 4.2.1.11).
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=89079778; PubMed=2462567; DOI=10.1083/jcb.107.6.2729;
RA Wistow G.J., Lieberman T., Williams L.A., Stapel S.O., de Jong W.W.,
RA Horwitz J., Platigorsky J.,
RT "Tau-crystallin/alpha-enolase: one gene encodes both an enzyme and a
RT lens structural protein.",
J. Cell Biol. 107:2729-2736 (1988).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=91365245; PubMed=1889745; DOI=10.1016/0378-1119(91)90273-E;
RX Kim R.Y., Belkman T., Platigorsky J., Wistow G.J.,
RT "Structure and expression of the duck alpha-enolase/-tau-crystallin-
RT encoding gene.",
Gene 103:193-200 (1991).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC EMBL: M55143; AAA49217.1, -, Genomic_DNA.
DR EMBL: M55134; AAA49217.1, JOINED; Genomic_DNA.
DR EMBL: M55135; AAA49217.1, JOINED; Genomic_DNA.
DR EMBL: M55136; AAA49217.1, JOINED; Genomic_DNA.
DR EMBL: M55138; AAA49217.1, JOINED; Genomic_DNA.
DR EMBL: M55140; AAA49217.1, JOINED; Genomic_DNA.
DR EMBL: M55142; AAA49217.1, JOINED; Genomic_DNA.
DR EMBL: M55141; AAA49217.1, JOINED; Genomic_DNA.
DR EMBL: M55139; AAA49217.1, JOINED; Genomic_DNA.
DR EMBL: M55137; AAA49217.1, JOINED; Genomic_DNA.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC GO: GO:0000015, C:phosphopyruvate hydratase complex, IEA.
DR GO: GO:0016829, P:lyase activity, IEA.
DR GO: GO:0004634, F:phosphopyruvate hydratase activity, IEA.
DR GO: GO:0006096, P:glycolysis, IEA.
DR InterPro: IPR000941, Enolase.
DR Pfam: PF00113, Enolase_C_1.
DR Pfam: PF03952, Enolase_N_1.
DR PRINTS: PR00148, ENOLASE.
DR ProDom: PD000902, Enolase_1.
DR TIGRFAMs: TIGR01060, eno, 1.
DR PROSITE: PS00164, ENOLASE, 1.
SQ SEQUENCE 377 AA; 40856 MW; 64B2B35F0C17C0C6 CRC64;
```



Query Match 72.2%; Score 65; DB 2; Length 377;  
Best Local Similarity 81.2%; Pred. No. 0.042;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGAPC 16  
Db 327 LVVGLCTGQIKTGAPC 342

RESULT 12

Q9NG67\_9HEXA PRELIMINARY; PRT; 383 AA.  
AC Q9NG67;  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DE Enolase (Fragment).  
OS Tomocerus sp. jctjwsl.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Collembola; Arthropodea;  
OC Entomobryidae; Tomoceridae; Tomocerus.  
NCBI\_Taxid=111305;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RA Regier J.C., Shultz J.W.;  
RL Submitted (Apr-2000) to the EMBL/Genbank/DDAJ databases.  
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.  
CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing the dimer (By similarity).  
CC -1- PATHWAY: Glycolysis.  
CC -1- SUBUNIT: Homodimer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- SIMILARITY: Belongs to the enolase family.  
DR EMBL; AF258670; AAF72641.1; -; mRNA.  
DR HSSP; P56252; 1PD2.  
DR SMR; Q9NG67; 1-383.  
DR GO; GO:0000015; C:phosphopyruvate hydratase complex; IEA.  
DR GO; GO:0016829; F:lyase activity; IEA.  
DR GO; GO:0000287; F:magnesium ion binding; IEA.  
DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.  
DR InterPro; IPR000941; Enolase.  
DR Pfam; PF00113; Enolase\_C; 1.  
DR Pfam; PF03952; Enolase\_N; 1.  
DR PRINTS; PR00148; ENOLASE.  
DR ProDom; PD000902; Enolase; 1.  
DR TIGRFAMs; TIGR01060; eno; 1.  
DR PROSITE; PS00164; ENOLASE; 1.  
KW Glycolysis; Lyase; Magnesium.  
FT NON\_TER 1  
FT NON\_TER 383  
SQ SEQUENCE 383 AA; 41326 MW; 4523F005FEA5E579 CRC64;  
Query Match 72.2%; Score 65; DB 2; Length 383;  
Best Local Similarity 81.2%; Pred. No. 0.042;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGAPC 16  
Db 363 LVVGLCTGQIKTGAPC 378

RESULT 13  
Q9PTX6\_LAMRE PRELIMINARY; PRT; 394 AA.  
AC Q9PTX6;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Enolase-1 (Fragment).  
OS Name=enolase-1;  
OS Lampetra reissneri (Far Eastern brook lamprey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
OC Petromyzontiformes; Petromyzontidae; Lethenteron.  
NCBI\_Taxid=7753;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20063780; PubMed=10594174;  
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;  
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded genes".  
RL J. Mol. Evol. 49:729-735(1999).  
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.  
CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing the dimer (By similarity).  
CC -1- PATHWAY: Glycolysis.  
CC -1- SUBUNIT: Homodimer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- SIMILARITY: Belongs to the enolase family.  
DR EMBL; AB025329; BAA88482.1; -; mRNA.  
DR HSSP; P56252; 1PD2.  
DR SMR; Q9PTX6; 1-392.  
DR GO; GO:0000015; C:phosphopyruvate hydratase complex; IEA.  
DR GO; GO:0016829; F:lyase activity; IEA.  
DR GO; GO:0000287; F:magnesium ion binding; IEA.  
DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.  
DR InterPro; IPR000941; Enolase.  
DR Pfam; PF00113; Enolase\_C; 1.  
DR Pfam; PF03952; Enolase\_N; 1.  
DR PRINTS; PR00148; ENOLASE.  
DR ProDom; PD000902; Enolase; 1.  
DR TIGRFAMs; TIGR01060; eno; 1.  
DR PROSITE; PS00164; ENOLASE; 1.  
KW Glycolysis; Lyase; Magnesium.  
FT NON\_TER 1  
FT NON\_TER 394  
SQ SEQUENCE 394 AA; 42583 MW; BC585FE6C712A3D2 CRC64;

Query Match 72.2%; Score 65; DB 2; Length 394;  
Best Local Similarity 81.2%; Pred. No. 0.043;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTGQIKTGAPC 16  
Db 345 LVVGLCTGQIKTGAPC 360

RESULT 14  
ENO\_ALIMI STANDARD; PRT; 395 AA.  
AC P42897;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Fragment).  
OS Alligator mississippiensis (American alligator).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.  
NCBI\_Taxid=8496;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=94195794; PubMed=8146164;  
RA Hedges S.B.;  
RT "Molecular evidence for the origin of birds".  
RL Proc. Natl. Acad. Sci. U.S.A. 91:2621-2624(1994).  
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.  
CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing the dimer (By similarity).  
CC -1- PATHWAY: Glycolysis.  
CC -1- SUBUNIT: Homodimer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: Belongs to the enolase family.

```
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; L28078; AAA53671.1; -; mRNA.
DR PIR; I50026; I50026.
DR HSSP; P56252; 1PDZ.
DR SMK; P42897; 1-395.
DR InterPro; IPR000941; Enolase.
DR PANTHER; PTHR11902; Enolase; 1.
DR Pfam; PF00113; Enolase_C; 1.
DR Pfam; PF03952; Enolase_N; 1.
DR PRINTS; PR00148; ENOLASE.
DR ProDom; PD000902; Enolase; 1.
DR TIGRFAMs; TIGR01060; eno; 1.
DR PROSITE; PS00164; ENOLASE; 1.
KM Glycolysis; Lyase; Magnesium; Metal-binding.
FT ACT SITE 136 136
FT METAL 223 223 By similarity.
FT METAL 271 271 Magnesium (By similarity).
FT METAL 296 296 Magnesium (By similarity).
FT NON_TER 1 1 Magnesium (By similarity).
SQ SEQUENCE 395 AA; 42884 MW; B43E91228E9110B5 CRC64;

Query Match 72.2%; Score 65; DB 1; Length 395;
Best Local Similarity 81.2%; Pred. No. 0.043;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTCQIKTGAPC 16
Db 362 LVVGLCTGQIKTGAPC 377

RESULT 15
Q9USF7 EPTBU PRELIMINARY; PRT; 395 AA.
ID Q9USF7_
AC Q9USF7_
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Enolase (Fragment).
OS Eptarectus burgeri (Inshore hagfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;
OC Myxiniidae; Eptarectinae; Eptarectus.
OX NCBI_TaxId=7764;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=20063780; PubMed=10594174;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
RT genes.";
RL J. Mol. Evol. 49:729-735(1999).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
CC H(2)O.
CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing
CC the dimer (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the enolase family.
DR EMBL; AB025326; BAA8479.1; -; mRNA.
DR HSSP; P56252; 1PDZ.
DR SMK; Q9USF7; 1-392.
DR GO; GO:000015; C:phosphopyruvate hydratase complex; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
```

```
DR InterPro; IPR000941; Enolase.
DR Pfam; PF00113; Enolase_C; 1.
DR Pfam; PF03952; Enolase_N; 1.
DR PRINTS; PR00148; ENOLASE.
DR ProDom; PD000902; Enolase; 1.
DR TIGRFAMs; TIGR01060; eno; 1.
DR PROSITE; PS00164; ENOLASE; 1.
KM Glycolysis; Lyase; Magnesium.
FT NON_TER 1 1
SQ SEQUENCE 395 AA; 43131 MW; D351C670DDC75CD CRC64;

Query Match 72.2%; Score 65; DB 2; Length 395;
Best Local Similarity 81.2%; Pred. No. 0.043;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTCQIKTGAPC 16
Db 345 LVVGLCTGQIKTGAPC 360
```

```
RESULT 16
Q9PTX5 LAMRE PRELIMINARY; PRT; 395 AA.
ID Q9PTX5_
AC Q9PTX5_
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Enolase-2 (Fragment).
GN Name=enolase-2;
OS Lampetra reissneri (Par Eastern brook lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Lethenteron.
OX NCBI_TaxId=7753;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20063780; PubMed=10594174;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
RT genes.";
RL J. Mol. Evol. 49:729-735(1999).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
CC H(2)O.
CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing
CC the dimer (By similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the enolase family.
DR EMBL; AB025330; BAA8483.1; -; mRNA.
DR HSSP; P56252; 1PDZ.
DR SMK; Q9PTX5; 1-394.
DR GO; GO:000015; C:phosphopyruvate hydratase complex; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR000941; Enolase.
DR Pfam; PF00113; Enolase_C; 1.
DR Pfam; PF03952; Enolase_N; 1.
DR PRINTS; PR00148; ENOLASE.
DR ProDom; PD000902; Enolase; 1.
DR TIGRFAMs; TIGR01060; eno; 1.
DR PROSITE; PS00164; ENOLASE; 1.
KM Glycolysis; Lyase; Magnesium.
FT NON_TER 1 1
SQ SEQUENCE 395 AA; 43267 MW; 8591D68662DA8544 CRC64;

Query Match 72.2%; Score 65; DB 2; Length 395;
Best Local Similarity 81.2%; Pred. No. 0.043;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTCQIKTGAPC 16
```

DB 345 LVWGLCTGQIKTGAPC 360

RESULT 17  
Q4SZW2\_TETNG PRELIMINARY; PRT; 406 AA.

AC Q4SZW2;  
DT 13-SEP-2005 (TREMBlrel. 31, Created)  
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
DE 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
DE Chromosome undetermined SCAF11462, whole genome shotgun sequence.  
GN ORFNAMES=GSTENG0009644001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OK NCBI\_TaxId=99883;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,  
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Nicud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
RA Daasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,  
RA Blemont C., Skalli Z., Catolico L., Poulain J., De Bernardis V.,  
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Guzy J.,  
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Landet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
RA Winkler P., Lander E.S., Weissbach J., Roest Crollins H.,  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype.",  
RL Nature 431:946-957(2004).  
RN (2)  
RP NUCLEOTIDE SEQUENCE.  
RG Genoscope; Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -! CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; CA01011462; CAF93820.1; -; Genomic DNA.  
SQ SEQUENCE 406 AA; 4372 MW; 18C266C4F923E27D CRC64;

Query Match 72.2%; Score 65; DB 2; Length 406;  
Best Local Similarity 81.2%; Pred. No. 0.044;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVWGLCTGQIKTGAPC 16  
DB 358 LVWGLCTGQIKTGAPC 373

RESULT 18  
OSIS00\_MACPA PRELIMINARY; PRT; 420 AA.

AC OSIS00;  
DT 10-MAY-2005 (TREMBlrel. 30, Created)  
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)  
DE 10-MAY-2005 (TREMBlrel. 30, Last annotation update)  
DE Enolase 2 (Fragment)  
OS Macaca fascicularis (Crisp eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
OC Cercopithecoidea; Cercopithecoidea; Macaca.  
OK NCBI\_TaxId=9541;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RA Pubmed15620360; DOI=10.1016/j.cell.2004.11.040;  
RA Doris S., Vallender E.J., Evans P.D., Anderson J.R., Gilbert S.L.,  
RA Mahowald M., Wyckoff G.J., Malcom C.M., Lahn B.T.,  
RT "Accelerated evolution of nervous system genes in the origin of Homo  
RT

RT sapiens.",  
RL Cell 119:1027-1040(2004).  
CC -! CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +  
CC H(2)O.  
CC -! COFACTOR: Magnesium. Required for catalysis and for stabilizing  
CC the dimer (By similarity).  
CC -! PATHWAY: Glycolysis.  
CC -! SUBUNIT: Homodimer (By similarity).  
CC -! SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -! SIMILARITY: Belongs to the enolase family.  
DR EMBL; AY650330; AAV67362.1; -; mRNA.  
DR SMR; Q51S00; 1-420.  
DR GO; GO:0000015; C:phosphopyruvate hydratase complex; IEA.  
DR GO; GO:0016829; F:lyase activity; IEA.  
DR GO; GO:0000287; F:magnesium ion binding; IEA.  
DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.  
DR GO; GO:0006096; P:glycolysis; IEA.  
DR InterPro; IPR000941; Enolase.  
DR Pfam; PF00113; Enolase\_C; 1.  
DR Pfam; PF03952; Enolase\_N; 1.  
DR PRINTS; PR00148; ENOLASE.  
DR ProDom; PD000902; Enolase; 1.  
DR TIGRPFAMs; TIGR01060; eno; 1.  
DR PROSITE; PS00164; ENOLASE; 1.  
KW Glycolysis; Lyase; Magnesium.  
FT NON\_TER 1  
FT 420  
SQ SEQUENCE 420 AA; 45540 MW; 0FF7DC4035539747 CRC64;

Query Match 72.2%; Score 65; DB 2; Length 420;  
Best Local Similarity 81.2%; Pred. No. 0.046;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVWGLCTGQIKTGAPC 16  
DB 377 LVWGLCTGQIKTGAPC 392

RESULT 19  
Q4TBD1\_TETNG PRELIMINARY; PRT; 431 AA.

AC Q4TBD1;  
DT 13-SEP-2005 (TREMBlrel. 31, Created)  
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
DE Chromosome undetermined SCAF7145, whole genome shotgun sequence.  
DE (Fragment).  
GN ORFNAMES=GSTENG0003809001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OK NCBI\_TaxId=99883;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,  
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Nicud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
RA Daasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,  
RA Blemont C., Skalli Z., Catolico L., Poulain J., De Bernardis V.,  
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Guzy J.,  
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Landet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
RA Winkler P., Lander E.S., Weissbach J., Roest Crollins H.,  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype.",  
RL Nature 431:946-957(2004).  
RN (2)  
RP NUCLEOTIDE SEQUENCE.

```
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
CC H(2)O.
CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing
CC the dimer (by similarity).
CC -1- PATHWAY: Glycolysis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the enolase family.
DR EMBL; CA601007145; CAF89801.1; -; Genomic_DNA.
DR InterPro; IPR000941; Enolase.
DR Pfam; PF00113; Enolase_C; 1.
DR Pfam; PF03952; Enolase_N; 1.
DR PRINTS; PR00148; ENOLASE.
DR PRODOM; PD000902; Enolase; 1.
DR TIGRFAMs; TIGR01060; eno; 1.
DR PROSITE; PS00164; ENOLASE; 1.
DR GlycoLyse; Lyase; Magnesium.
FT NON_TER 431 431
SQ SEQUENCE 431 AA; 47111 MW; BFA79F670744BC1 CRC64;

Query Match 72.2%; Score 65; DB 2; Length 431;
Best Local Similarity 81.2%; Pred. No. 0.047;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
Db 384 LVVGLCTGQIKTGAPC 399

RESULT 20
Q610P5_BRARE PRELIMINARY; PRT; 432 AA.
ID Q610P5_BRARE PRELIMINARY; PRT; 432 AA.
AC Q610P5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Enolase 1, (Alpha).
GN ORFNames=zgc:73152;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullany S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
```

```
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Director MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC071359; AAH71359.1; -; mRNA.
DR SMR; Q6PC12; 2-431.
DR ZFIN; ZDB-GENE-030131-6048; zgc:73152.
DR GO; GO:000015; C:phosphopyruvate hydratase complex; IEA.
DR GO; GO:0004634; F:phosphopyruvate hydratase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR000941; Enolase.
DR Pfam; PF00113; Enolase_C; 1.
DR Pfam; PF03952; Enolase_N; 1.
DR PRINTS; PR00148; ENOLASE.
DR PRODOM; PD000902; Enolase; 1.
DR TIGRFAMs; TIGR01060; eno; 1.
DR PROSITE; PS00164; ENOLASE; 1.
DR PROSITE; PS00164; ENOLASE; 1.
SQ SEQUENCE 432 AA; 47059 MW; F743FC00CD249F6F CRC64;

Query Match 72.2%; Score 65; DB 2; Length 432;
Best Local Similarity 81.2%; Pred. No. 0.047;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
Db 384 LVVGLCTGQIKTGAPC 399

RESULT 21
Q6PC12_BRARE PRELIMINARY; PRT; 432 AA.
ID Q6PC12_BRARE PRELIMINARY; PRT; 432 AA.
AC Q6PC12;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Enolase 1, (Alpha).
GN ORFNames=zgc:73152;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Wild-type; TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullany S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Wild-type; TISSUE=Eye;
RA Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC059511; AAH59511.1; -; mRNA.
DR SMR; Q6PC12; 2-431.
```



Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16

DB 383 LVVGLCTGQIKTGAPC 398

## RESULT 24

ENOA\_CHICK STANDARD; PRT; 433 AA.

AC P51913.

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)

DE (Phosphopyruvate hydratase).

GN Name=ENO1.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OC NCBI\_TaxID=9031;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=White Leghorn; TISSUE=Kidney;

RX MEDLINE=9355305; PubMed=7629021;

RA Tanaka M., Maeda K., Nakashima K.;

RT "Chicken alpha-enolase but not beta-enolase has a Src-dependent tyrosine-phosphorylation site: cDNA cloning and nucleotide sequence analysis.";

RT J. Biochem. 117:554-559 (1995).

CC -1- CATALYTIC ACTIVITY. 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.

CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing the dimer (by similarity).

CC -1- PATHWAY: Glycolysis.

CC -1- SUBUNIT: Homodimer (by similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: Belongs to the enolase family.

CC -----

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CC

DR EMBL; D37900; BAA07132.1; -; mRNA.

DR PIR; JCA186; JCA186.

DR HSSP; P56252; IPDZ.

DR SMR; P51913; 1-432.

DR Ensembl; ENSGALG0000014528; Gallus gallus.

DR InterPro; IPR000941; Enolase.

DR PANTHER; PTHR11902; Enolase; 1.

DR Pfam; PF00113; Enolase\_C; 1.

DR Pfam; PF03952; Enolase\_N; 1.

DR PRINTS; PR00148; ENOLASE.

DR ProDom; PD000902; Enolase; 1.

DR TIGRFAMs; TIGR01060; eno; 1.

DR PROSITE; PS00164; ENOLASE; 1.

KW Glycolysis; Lyase; Magnesium; Metal-binding; Multigene family.

FT INIT MET 0

FT ACT SITE 157

FT METAL 157

FT METAL 244

FT METAL 292

FT METAL 317

SO SEQUENCE 433 AA; 47174 MW; 93AD6B0A7AD99910 CRC64;

Query Match 72.2%; Score 65; DB 1; Length 433;

Best Local Similarity 81.2%; Pred. No. 0.047;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16

DB 383 LVVGLCTGQIKTGAPC 398

## RESULT 25

ENOA\_HUMAN STANDARD; PRT; 433 AA.

AC P06733; P22712; Q16704; Q658M5; Q6GMP2; Q71V37; Q723V6; Q8MU71;

AC Q9UM55;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-APR-1988 (Rel. 07, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1) (Phosphopyruvate hydratase) (C-myc promoter-binding protein) (MPB-1) (MPB-1) (Plasminogen-binding protein).

GN Name=ENO1; Synonyms=ENO1L1, MBP1, MPB1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

OC NCBI\_TaxID=9606;

OK

RN [1]

RP NUCLEOTIDE SEQUENCE (ISOFORM ALPHA-ENOLASE).

RX MEDLINE=86313654; PubMed=3529090;

RA Galliono A., Feo S., Moore R., Croce C.M., Showne L.C.;

RT "Molecular cloning and nucleotide sequence of a full-length cDNA for human alpha enolase.";

RL Proc. Natl. Acad. Sci. U.S.A. 83:6741-6745 (1986).

RN [2]

RP NUCLEOTIDE SEQUENCE (ISOFORM ALPHA-ENOLASE).

RX MEDLINE=90323004; PubMed=2373081;

RA Galliono A., Oliva D., Cali L., Barba G., Barbieri G., Feo S.;

RT "Structure of the human gene for alpha-enolase.";

RL Eur. J. Biochem. 190:567-573 (1990).

RN [3]

RP NUCLEOTIDE SEQUENCE (ISOFORM MBP-1), AND FUNCTION.

RX MEDLINE=91172204; PubMed=2005901;

RA Ray R., Miller D.M.;

RT "Cloning and characterization of a human c-myc promoter-binding protein.";

RT Mol. Cell. Biol. 11:2154-2161 (1991).

RN [4]

RP NUCLEOTIDE SEQUENCE (ISOFORM ALPHA-ENOLASE), AND MARKER FOR ENDOMETRIOSIS.

RX MEDLINE=96422099; PubMed=8824716;

RA Walter M., Leidenberger F.A., Schweppe K.W., Berg H., Northmann W.;

RT "Auto-reactive epitopes within the human alpha-enolase and their recognition by sera from patients with endometriosis.";

RL J. Autoimmun. 8:937-945 (1995).

RN [5]

RP NUCLEOTIDE SEQUENCE (ISOFORM ALPHA-ENOLASE).

RA Frankland J.;

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

RN [6]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM ALPHA-ENOLASE).

RC TISSUE=Retina, and Stomach;

RX The German cDNA consortium;

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

RN [7]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM ALPHA-ENOLASE).

RC TISSUE=Brain, Eye, Lung, Ovary, Pancreatic carcinoma, and Skin;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Ustin T.B., Toshitoki S., Carrinci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullaly S.J., Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Heiton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,  
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [8]  
 RN NUCLEOTIDE SEQUENCE OF 165-433.  
 RX MEDLINE=98317532; PubMed=9653645; DOI=10.1006/geno.1997.5186;  
 RA Onyango P., Lubyova B., Gardellin P., Kurzbauer R., Welch A.,  
 RT "Molecular cloning and expression analysis of five novel genes in  
 RT chromosome 1p36.";  
 RT Genomics 50:187-198(1998).  
 RN [9]  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 170-433.  
 RC TISSUE=Brain;  
 RX MEDLINE=97264341; PubMed=9110174;  
 RA Yu W., Andersen B., Worley K.C., Muzny D.M., Ding Y., Liu W.,  
 RA Ricafrente J.Y., Wentland M.A., Lennon G., Gibbs R.A.,  
 RT "Large-scale concatenation cDNA sequencing.";  
 RT Genome Res. 7:353-358(1997).  
 RN [10]  
 RN PROTEIN SEQUENCE OF 269-280 AND 306-320, AND INDUCTION IN DIFFUSE  
 RP LARGE CELL LYMPHOMA.  
 RX MEDLINE=95307657; PubMed=7787969;  
 RA Mohamed R.M., Hamdan M.Y., Maki A., Al-Katib A.,  
 RT "Induced expression of alpha-enolase in differentiated diffuse large  
 RT cell lymphoma.";  
 RT Enzyme Protein 48:37-44(1995).  
 RN [11]  
 RN PROTEIN SEQUENCE OF 1-8 (ISOFORM ALPHA-ENOLASE).  
 RC TISSUE=Colon carcinoma;  
 RX MEDLINE=97295306; PubMed=9150948;  
 RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.,  
 RT "A two-dimensional gel database of human colon carcinoma proteins.";  
 RT Electrophoresis 18:605-613(1997).  
 RN [12]  
 RN FUNCTION OF MBP1, IDENTIFICATION OF REPRESSOR DOMAINS, AND MUTAGENESIS  
 RP OF LEU-383 AND LEU-387.  
 RX MEDLINE=99182475; PubMed=10082554;  
 RA Ghosh A.K., Steele R., Ray R.B.,  
 RT "Functional domains of c-myc promoter binding protein 1 involved in  
 RT transcriptional repression and cell growth regulation.";  
 RT Mol. Cell. Biol. 19:2880-2886(1999).  
 RN [13]  
 RN FUNCTION AS A C-MYC TRANSCRIPTIONAL REPRESSOR, AND SUBCELLULAR  
 RP LOCATION.  
 RX MEDLINE=20263726; PubMed=10802057; DOI=10.1016/S0014-5793(00)01494-0;  
 RA Feo S., Arcuri D., Piddini E., Pasantino R., Gallongo A.,  
 RT "EN1 gene product binds to the c-myc promoter and acts as a  
 RT transcriptional repressor: relationship with Myc promoter-binding  
 RT protein 1 (MBP-1)."  
 RT FEBS Lett. 473:47-52(2000).  
 RN [14]  
 RN FUNCTION IN PLASMINOGEN ACTIVATION.  
 RX MEDLINE=22551878; PubMed=1266133; DOI=10.1002/ajh.10299;  
 RA Lopez-Alemay R., Longstaff C., Hawley S., Mirshahi M., Fabregas P.,  
 RA Tardif M., Meron E., Miles L.A., Felez J.,  
 RT "Inhibition of cell surface mediated plasminogen activation by a  
 RT monoclonal antibody against alpha-enolase.";  
 RT Am. J. Hematol. 72:234-242(2003).  
 RN [15]  
 RN INTERACTION WITH PLG.  
 RP MEDLINE=97452346; PubMed=9308760;  
 RX Arza B., Felez J., Lopez-Alemay R., Miles L.A., Munoz-Caroves P.,  
 RT "Identification of an epitope of alpha-enolase (a candidate  
 RT plasminogen receptor) by phage display.";  
 RT Thromb. Haemost. 78:1097-1103(1997).  
 RN [16]

RP EPIPEPE MAPPING, AND ASSOCIATION WITH CAR.  
 RX MEDLINE=99096529; PubMed=9878089; DOI=10.1006/jaut.1998.0239;  
 RA Adams G., Amundson D., Seigel G.M., Machnicki M.,  
 RT "Anti-enolase-alpha autoantibodies in cancer-associated retinopathy:  
 RT epitope mapping and cytotoxicity on retinal cells.";  
 RT J. Autoimmun. 11:671-677(1998).  
 RN [17]  
 RN IDENTIFICATION OF MBP1 AS AN ALPHA ENOLASE ALTERNATIVE INITIATION  
 RP PRODUCT AND MUTAGENESIS OF MET-93 AND MET-96.  
 RX MEDLINE=20148810; PubMed=10681589; DOI=10.1074/jbc.275.8.5958;  
 RA Subramanian A., Miller D.M.,  
 RT "Structural analysis of alpha-enolase. Mapping the functional domains  
 RT involved in down-regulation of the c-myc protooncogene.";  
 RT J. Biol. Chem. 275:5958-5965(2000).  
 RN [18]  
 RN REVIEW.  
 RX MEDLINE=21388199; PubMed=11497239,  
 RA Pancholi V.,  
 RT "Multifunctional alpha-enolase: its role in diseases.";  
 RT Cell. Mol. Life Sci. 58:902-920(2001).  
 RN [19]  
 RP INTERACTION OF MBP1 WITH SBDL.  
 RX MEDLINE=20576881; PubMed=11134351; DOI=10.1128/MCB.21.2.655-662.2001;  
 RA Ghosh A.K., Majumder M., Steele R., White R.A., Ray R.B.,  
 RT "A novel 16-kilodalton cellular protein physically interacts with and  
 RT antagonizes the functional activity of c-myc promoter-binding protein  
 RT 1.";  
 RT Mol. Cell. Biol. 21:655-662(2001).  
 RN [20]  
 RN IDENTIFICATION AS AN AUTOANTIGEN IN HASHIMOTO ENCEPHALOPATHY.  
 RX MEDLINE=22237360; PubMed=12297304; DOI=10.1016/S0014-5793(02)03307-0;  
 RA Ochi H., Horinchi I., Araki N., Toda T., Araki T., Sato K., Murali H.,  
 RA Oosagawa M., Yamada T., Okamura K., Ogino T., Mizumoto K.,  
 RA Yamaehita H., Sawa H., Kira J.,  
 RT "Proteomic analysis of human brain identifies alpha-enolase as a novel  
 RT autoantigen in Hashimoto's encephalopathy.";  
 RT FEBS Lett. 528:197-202(2002).  
 RN [21]  
 RN FUNCTION: Multifunctional enzyme that, as well as its role in  
 CC glycolysis, plays a part in various processes such as growth  
 CC control, hypoxia tolerance and allergic responses. May also  
 CC function in the intravascular and pericellular fibrinolytic system  
 CC due to its ability to serve as a receptor and activator of  
 CC plasminogen on the cell surface of several cell-types such as  
 CC leukocytes and neurons.  
 CC -1- FUNCTION: MBP1 binds to the c-myc promoter and acts as a  
 CC transcriptional repressor. May be a tumor suppressor.  
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +  
 CC H(2)O.  
 CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing  
 CC the dimer.  
 CC -1- PATHWAY: Glycolysis.  
 CC -1- SUBUNIT: Mammalian enolase is composed of 3 isozyme subunits,  
 CC alpha, beta and gamma, which can form homodimers or heterodimers  
 CC which are cell-type and development-specific. EN1 interacts with  
 CC PLG in the neuronal plasma membrane and promotes its activation.  
 CC The C-terminal lysine is required for this binding (By  
 CC similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Can translocate to the plasma  
 CC membrane in either the homodimeric (alpha/alpha) or heterodimeric  
 CC (alpha/beta) form.

Query Match 72.2%; Score 65; DB 1; Length 433;  
 Best Local Similarity 81.2%; Pred. No. 0.047;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 LVVGLCTCQIKTGPAC 16  
 383 LVVGLCTCQIKTGPAC 398

RESULT 26  
 ENOA\_MOUSE STANDARD; PRT; 433 AA.  
 ID ENOA\_MOUSE  
 AC P17182; Q99KT7; Q9DCV7;



DT 01-AUG-1990 (Rel. 15, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-  
 DE neutral enolase) (NNE) (Enolase 1).  
 GN Name=Eno1; Synonyms=Eno-1;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OK NCBI\_TaxId=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=90301487; PubMed=2362815;  
 RA Kashad M., Dumont X., Chalton P., Lelias J.M., Lamande N., Lucas M.,  
 RA Lazar M., Caput D.;  
 RT "Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from  
 RT mouse brain";  
 RL Nucleic Acids Res. 18:3638-3638 (1990).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).  
 RC STRAIN=C57BL/6J; TISSUE=Kidney;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaido I., Otsu N., Saito R., Suzuki H., Yamana K.I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quakenbush J.,  
 RA Schmitt L.M., Kaplan A., Matcova H., Batilov S., Betsel K.W.,  
 RA Datta E., Dragan T.A., Fletcher C.F., Forrest A., Fraser K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Corbali L.E., Cousins S.,  
 RA Grimmond S., Gustinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.D., Qi D., Ramchandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sautelin A., Schneider C., Sempell C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wrynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hitotane-Kishikawa T., Kono H., Nakamura M., Sato K.,  
 RA Shitaki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Ysunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573 (2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).  
 RC STRAIN=Czech II, and FVB/N; TISSUE=Mammary gland, and Mammary tumor;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klauer R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Umed T.B., Toshlyuk S., Carninci P., Prange C.,  
 RA Bosa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [4]  
 RP PROTEIN SEQUENCE OF 59-70; 99-113; 183-197 AND 245-258.  
 RC TISSUE=Macrophage;  
 RX PubMed=8427861;  
 RA Bortolico L.A., Kendrick N.C., Keller A., Li Y., Tabas I.;  
 RT "Cholesteryl ester loading of mouse peritoneal macrophages is  
 RT associated with changes in the expression or modification of specific  
 RT cellular proteins, including increase in an alpha-enolase isoform";  
 RL Atheroscler. Thromb. 13:264-275 (1993).  
 RN [5]  
 RP INTERACTIONS WITH PKM2; PKM; CKM; ALDO AND TROPONIN, AND DEVELOPMENTAL  
 RP STAGE.  
 RX MEDLINE=97270626; PubMed=919614;  
 RA Merkulova T., Lucas M., Jabet C., Lamande N., Rouzeau J.-D., Gros F.,  
 RA Lazar M., Keller A.;  
 RT "Biochemical characterization of the mouse muscle-specific enolase:  
 RT developmental changes in electrophoretic variants and selective  
 RT binding to other proteins";  
 RL Biochem. J. 323:791-800 (1997).  
 RN [6]  
 RP SUBCELLULAR LOCATION AND TISSUE SPECIFICITY.  
 RX MEDLINE=21121273; PubMed=11229603; DOI=10.1016/S0248-4900(00)01103-5;  
 RA Keller A., Demeure J., Merkulova T., Gerard G., Cywiler-Golenzner C.,  
 RA Lucas M., Chatelet F.-P.;  
 RT "Fibre-type distribution and subcellular localisation of alpha and  
 RT beta enolase in mouse striated muscle";  
 RL Biol. Cell 92:527-535 (2000).  
 CC -1- FUNCTION: Multifunctional enzyme that, as well as its role in  
 CC glycolysis, plays a part in various processes such as growth  
 CC control, hypoxia tolerance and allergic responses (By similarity).  
 CC May also function in the intravascular and pericellular  
 CC fibrinolytic system due to its ability to serve as a receptor and  
 CC activator of plasminogen on the cell surface of several cell-types  
 CC such as leukocytes and neurons (By similarity).  
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +  
 CC H(2)O.  
 CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing  
 CC the dimer.  
 CC -1- PATHWAY: Glycolysis.  
 CC -1- SUBUNIT: Mammalian enolase is composed of 3 isozyme subunits,  
 CC alpha, beta and gamma, which can form homodimers or heterodimers  
 CC which are cell-type and development-specific. ENO1 interacts with  
 CC PLG in the neuronal plasma membrane and promotes its activation.  
 CC The C-terminal lysine is required for this binding (By  
 CC similarity). In vitro, interacts with several glycolytic enzymes  
 CC including PKM2, PKM, CKM and aldolase. Also binds troponin, in  
 CC vitro.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Can translocate to the plasma  
 CC membrane in either the homodimeric (alpha/alpha) or heterodimeric  
 CC (alpha/gamma) form (By similarity). ENO1 is localized to the M-  
 CC band.  
 CC -1- TISSUE SPECIFICITY: The alpha/alpha homodimer is expressed in  
 CC embryo and in most adult tissues. The alpha/beta heterodimer and  
 CC the beta/beta homodimer are found in striated muscle, and the  
 CC alpha/gamma heterodimer and the gamma/gamma homodimer in neurons.  
 CC In striated muscle, expression of ENO1 appears to be independent  
 CC of fiber type.  
 CC -1- DEVELOPMENTAL STAGE: During ontogenesis, there is a transition  
 CC from the alpha/alpha homodimer to the alpha/beta heterodimer in  
 CC striated muscle cells, and to the alpha/gamma heterodimer in nerve  
 CC cells. In embryonic muscle, ENO1 is highly expressed until E17.  
 CC -1- SIMILARITY: Belongs to the enolase family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.



CC	EMBL	Accession	Gene	Feature	Product	Protein	Enzyme	EC	Ref	Notes
CC	EMBL	X52379	CAN36605.1	-	mrna					
DR	EMBL	AK002336	BAB22022.1	-	mrna					
DR	EMBL	BC003891	AAH03891.1	-	mrna					
DR	EMBL	BC004017	AAH04017.1	-	mrna					
DR	EMBL	BC010685	AAH10685.1	-	mrna					
DR	EMBL	BC024644	AAH24644.1	-	mrna					
DR	EMBL	BC085098	AAH85098.1	-	mrna					
DR	PIR	S10246	S10246	-						
DR	HSSD	P56252	IPDZ	-						
DR	SMR	P17182	1-430	-						
DR	IntAct	P17182	-	-						
DR	SWISS-2DPAGE	P17182	MOUSE	-						
DR	MGI	MGI:95393	Enol	-						
DR	GO	GO:0005515	F:protein binding	-						
DR	InterPro	IPR000941	Enolase	-						
DR	PANTHER	PTHR11902	Enolase	-						
DR	Pfam	PF00113	Enolase_C	-						
DR	Pfam	PF03952	Enolase_N	-						
DR	PRINTS	PR00148	ENOLASE	-						
DR	ProDom	PD000902	Enolase	-						
DR	TIGRfam	TIGR01060	eno	-						
DR	PROSITE	PS00164	ENOLASE	-						
KW	Direct protein sequencing		Glycolysis	-						
KW	Metal-binding		Multigene family	-						
FT	INIT MET	0		-						
FT	REGION	404	433	-						
FT	ACT_SITE	157	157	-						
FT	METAL	244	244	-						
FT	METAL	292	292	-						
FT	METAL	317	317	-						
FT	CONFLICT	358	358	-						
SO	SEQUENCE	433 AA	47010 MW	-						

	CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - CC the European Bioinformatics Institute. There are no restrictions on its CC use as long as its content is in no way modified and this statement is not removed.		CC
	DR	EMBL; AF072589; AAD41646.1; -, mRNA.		CC
	DR	HSSP; P56252; IPDZ.		CC
	DR	SMR; Q9W7L0; 1-432.		CC
	DR	InterPro; IPR000941; Enolase.		CC
	DR	PANTHER; PTHR11902; Enolase; 1.		CC
	DR	pfam; PF00113; Enolase_C; 1.		CC
	DR	pfam; PF03952; Enolase_N; 1.		CC
	DR	PRINTS; PR00148; ENOLASE.		CC
	DR	PRODOM; PD000902; Enolase; 1.		CC
	DR	TIGRFAMs; TIGR01060; eno; 1.		CC
	DR	PROSITE; PS00164; ENOLASE; 1.		CC
KM	GLYCOLYSIS; lyase; Magnesium; Metal-binding; Multigene family.			
FT	INT MET 0 0 By similarity.			
FT	METAL 244 244 Magnesium (By similarity).			
FT	METAL 292 292 Magnesium (By similarity).			
FT	METAL 317 317 Magnesium (By similarity).			
SQ	SEQUENCE 433 AA; 47439 MW; E0AD198562629D23 CRC64;			
Query Match	72.2%; Score 65; DB 1; Length 433;			
Bee Local Similarity	81.2%; Pred. No. 0.047;			
Matches 13; Conservative	0; Mismatches 3; Indels 0; Gaps 0;			
Oy	1 LVVGLCTGQIKTGAPC 16           Db 383 LVVGLCTGQIKTGPC 398			

	Query Match	Best Local Similarity	72.2%	Score 65;	DB 1;	Length 433;
	Matches	13; Conservative	81.2%	Pred. No. 0.047;		
		0;	Mismatches	3;	Indels	0;
					Gaps	0;
QY	1 LVVGLCTGQIKTGPAC	16				
DB	383 LVVGLCTGQIKTGPAC	398				
RESULT 27						
ENOA_PYTRG						
ID	ENOA_PYTRG	STANDARD;	PRT;	433	AA.	
AC	Q9W710;					
DT	28-FEB-2003 (Rel. 41, Created)					
DT	28-FEB-2003 (Rel. 41, Last sequence update)					
DT	13-SEP-2005 (Rel. 48, Last annotation update)					
DE	Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)					
OS	(Phosphoglycerate hydratase).					
DE	Pythou regius (ball pythou) (Royal pythou).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Lepidodonta; Squamata; Scleroglossa; Serpentes; Hemophidia;					
OC	Pythouidae; Pythou.					
OX	NCBI_TextID=51751;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					
RC	TISSUE=Muscle;					
RA	MEBLIN=99439677; PubMed=10508547; DOI=10.1006/mpcv.1999.0640;					
RA	Mann H., Li S.-L.;					
RT	Mol. Phylogenet. Evol. 13:144-148(1999).					
RL	Mol. Phylogenet. Evol. 13:144-148(1999).					
CC	-1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +					
CC	H(2)O.					
CC	-1- Cofactor: Magnesium. Required for catalysis and for stabilizing					
CC	the dimer (by similarity).					
CC	-1- PATHWAY: Glycolysis.					
CC	-1- SUBUNIT: Homodimer (By similarity).					
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.					
CC	-1- SIMILARITY: Belongs to the enolase family.					

ID	ENOA_RAT	STANDARD:	PRT:	433 AA.
AC	P04764;	Q66H13; Q6ATV3; Q6P504;		
DT	13-AUG-1987	(Rel. 05, Created)		
DT	01-FEB-2005	(Rel. 46, Last sequence update)		
DT	13-SEP-2005	(Rel. 48, Last annotation update)		
DE	Alpha enolase (BC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1).			
GN	Name=Eno1; Synonyms=Eno-1;			
OC	Rattus norvegicus (Rat).			
OC	Karyote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Microidea; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Brain, and Liver;			
RX	MEDLINE=85242108; PubMed=2989793; Sakimura K., Kushiyama E., Obinata M., Takahashi Y.,			
RT	"Molecular cloning and the nucleotide sequence of cDNA to mRNA for non-neuronal enolase (alpha alpha enolase) of rat brain and liver.";			
RL	Nucleic Acids Res. 13:4365-4378(1985).			
RN	[2]			
RP	SEQUENCE REVISION.			
RA	Takahashi Y.;			
RL	Submitted (VAN-1986) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].			
RC	TISSUE=Heart, Pituitary, and Testis;			
RG	NH - Mammalian Gene Collection (MGC) project;			
RL	Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE OF 92-152.			
RC	TISSUE=Lymphoma;			
RT	Bole-Reyrot C., Kelly P.A.;			
RL	"Rat cDNA encoding alpha enolase (2-phospho-D-glycerate hydro-lyase) (non-neural enolase) (NNE).";			
RL	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.			

[5]  
 RP PROTEIN SEQUENCE OF 45-56; 96-108; 244-261 AND 368-381, AND  
 RP INTERACTION WITH PLG.  
 RC TISSUE=embryonic brain;  
 RA MEDLINE=95054017; PubMed=7964722;  
 RA Nakajima K., Hamanoue M., Takemoto N., Hattori T., Kato K.,  
 RA Kohaka S.;  
 RT "Plasminogen binds specifically to alpha-enolase on rat neuronal  
 RT plasma membrane.";   
 RL J. Neurochem. 63:2048-2057(1994).  
 RN [6]  
 RP DEVELOPMENTAL STAGE.  
 RX MEDLINE=96134716; PubMed=8594891;  
 RA Kellier A., Rouzeau J.D., Farhadian F., Wisniewsky C., Marotte F.,  
 RA Lamande N., Samuel J.L., Schwartz K., Lazar M., Lucas M.;  
 RT "differential expression of alpha- and beta-enolase genes during rat  
 RT heart development and hypertrophy.";   
 RL Am. J. Physiol. 269:H1843-H1851(1995).  
 RN [7]  
 RP EFFECT OF THYROID HORMONES ON EXPRESSION.  
 RX MEDLINE=20131238; PubMed=10662718;  
 RA Merkulova T., Kellier A., Oliviero P., Marotte F., Samuel J.L.,  
 RA Rappaport L., Lamande N., Lucas M.;  
 RT "Thyroid hormones differentially modulate enolase isozymes during rat  
 RT skeletal and cardiac muscle development.";   
 RL Am. J. Physiol. 278:E330-E339(2000).  
 RN [8]  
 RP SUBCELLULAR LOCATION OF ALPHA/GAMMA HETERODIMER.  
 RX PubMed=15041191; DOI=10.1016/j.neures.2003.12.006.  
 RA Ueta H., Nagasawa H., Oyabu-Manabe Y., Toida K., Ishimura K., Hori H.;  
 RT "localization of enolase in synaptic plasma membrane as an alphasgamma  
 RT heterodimer in rat brain.";   
 RL Neurosci. Res. 48:379-386(2004).  
 CC -1- FUNCTION: Multifunctional enzyme that, as well as its role in  
 CC glycolysis, plays a part in various processes such as growth  
 CC control, hypoxia tolerance and allergic responses. May also  
 CC function in the intravascular and pericellular fibrinolytic system  
 CC due to its ability to serve as a receptor and activator of  
 CC plasminogen on the cell surface of several cell-types such as  
 CC leukocytes and neurons.  
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +  
 CC H(2)O.  
 CC -1- COPACITOR: Magnesium. Required for catalysis and for stabilizing  
 CC the dimer.  
 CC -1- PATHWAY: Glycolysis.  
 CC -1- SUBUNIT: Mammalian enolase is composed of 3 isozyme subunits,  
 CC alpha, beta and gamma, which can form homodimers or heterodimers  
 CC which are cell-type and development-specific. ENO1 interacts with  
 CC PLG in the neuronal plasma membrane and promotes its activation.  
 CC The C-terminal lysine is required for this binding (By  
 CC similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Can translocate to the plasma  
 CC membrane in either the homodimeric (alpha/alpha) or heterodimeric  
 CC (alpha/gamma) form.  
 CC -1- TISSUE SPECIFICITY: The alpha/alpha homodimer is expressed in  
 CC embryo and in most adult tissues. The alpha/beta heterodimer and  
 CC the beta/beta homodimer are found in striated muscle, and the  
 CC alpha/gamma heterodimer and the gamma/gamma homodimer in neurons.  
 CC -1- DEVELOPMENTAL STAGE: During ontogenesis, there is a transition  
 CC from the alpha/alpha homodimer to the alpha/beta heterodimer in  
 CC striated muscle cells, and to the alpha/gamma heterodimer in nerve  
 CC cells. In brain, levels of ENO1 decrease around 10 dpc and then  
 CC gradually increase to adult age. In embryonic heart, ENO1 levels  
 CC decrease rapidly during cardiac development.  
 CC -1- SIMILARITY: Belongs to the enolase family.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC EMBL; X02610; CAA26456.1; -, mRNA.

DR EMBL; BC063174; AA63174.1; ALT INIT; mRNA.  
 DR EMBL; BC078896; AA78896.1; -, mRNA.  
 DR EMBL; BC081847; AA81847.1; ALT INIT; mRNA.  
 DR EMBL; AF241613; AA801319.1; -, mRNA.  
 DR PIR; A23126; A23126.  
 DR HSP; P56252; 1P2.  
 DR SMK; P04764; 1-430.  
 DR Ensembl; ENSRNOG0000017895; Rattus norvegicus.  
 DR RGD; 2553; Enol.  
 DR InterPro; IPR000941; Enolase.  
 DR PANTHER; PTHR11902; Enolase; 1.  
 DR Pfam; PF00113; Enolase\_C; 1.  
 DR Pfam; PF03952; Enolase\_N; 1.  
 DR PRINTS; PR00148; ENOLASE.  
 DR ProDom; PD000902; Enolase; 1.  
 DR TIGRFAMs; TIGR01060; eno; 1.  
 DR PROSITE; PS00164; ENOLASE; 1.  
 DR Direct protein sequencing; Glycolysis; Lyase; Magnesium;  
 KW Metal-binding; Multigene Family; Plasminogen activation.  
 FT INIT MET 0  
 FT REGION 404 433  
 FT ACT SITE 157 157  
 FT METAL 244 244  
 FT METAL 292 292  
 FT METAL 317 317  
 FT CONFLICT 47 47  
 FT CONFLICT 92 95  
 FT CONFLICT 124 124  
 FT CONFLICT 143 143  
 FT CONFLICT 150 150  
 FT CONFLICT 249 249  
 FT CONFLICT 373 373  
 SQ SEQUENCE 433 AA; 46997 MW; 61898009DADCDBCC CRC64;  
 Query Match 72.2%; Score 65; DB 1; Length 433;  
 Best Local Similarity 81.2%; Pred. NO. 0.047;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 LVNGICTGQIKTPGK 16  
 Db 383 LVNGICTGQIKTPGK 398  
 RESULT 29  
 ENOA\_SCEUN STANDARD; PRT; 433 AA.  
 AC Q9W7L2;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)  
 DE (Phosphopyruvate hydratase).  
 OS Sceloporus undulatus (Eastern fence lizard) (Skink).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodonta; Squamata; Iguania; Iguanidae; Phrynosomatinae;  
 OC Sceloporus.  
 OX NCBI\_TaxID=8520;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Muscle;  
 RX MEDLINE=9943677; PubMed=10508547; DOI=10.1006/mpcv.1999.0640;  
 RA Mamen H., Li S.S.-L.;  
 RT "Molecular evidence for a clade of turtles.";   
 RL Mol. Phylogenet. Evol. 13:144-148(1999).  
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +  
 CC H(2)O.  
 CC -1- COPACITOR: Magnesium. Required for catalysis and for stabilizing  
 CC the dimer (By similarity).  
 CC -1- PATHWAY: Glycolysis.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: Belongs to the enolase family.  
 CC -----

CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.

CC -----  
DR EMBL: AF072587; AAD41644.1; -, mRNA.

DR HSSP: P56252; 1PDZ.

DR SMR: Q9W7L2; 1-432.

DR InterPro: IPR000941; Enolase.

DR PANTHER: PTHR11902; Enolase; 1.

DR Pfam: PF00113; Enolase\_C; 1.

DR Pfam: PF03952; Enolase\_N; 1.

DR PRINTS: PR00148; ENOLASE.

DR ProDom: PD000902; Enolase; 1.

DR TIGRPFAM: TIGR01060; eno; 1.

DR PROSITE: PS00164; ENOLASE; 1.

KW Glycolysis; Lyase; Magnesium; Metal-binding; Multigene family.

FT INIT MET 0 0 By similarity.

FT METAL 244 244 Magnesium (By similarity).

FT METAL 292 292 Magnesium (By similarity).

FT METAL 317 317 Magnesium (By similarity).

SQ SEQUENCE 433 AA; 47362 MW; 7CD89EB405529301 CRC64;

Query Match 72.2%; Score 65; DB 1; Length 433;

Best Local Similarity 81.2%; Pred. No. 0.047;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16

DB 383 LVVGLCTGQIKTGAPC 398

ENOA\_TRASC STANDARD; PRT; 433 AA.

ID ENO7L1;

AC Q9W7L1;

DT 28-FEB-2003 (Rel. 41; Created)

DT 28-FEB-2003 (Rel. 41; Last sequence update)

DT 13-SEP-2005 (Rel. 48; Last annotation update)

DE Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)

OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Testudines; Cryptodira; Testudinoidae; Emydidae; Trachemys.

NCBI\_TaxId=34903;

RN (1)

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Subsp. elegans; TISSUE=Muscle;

RX MEDLINE=99439677; PubMed=10508547; DOI=10.1006/mpev.1999.0640;

RA Mannen H., Li S.S.-L.;

RT "Molecular evidence for a clade of turtles.";

RL Mol. Phylogenet. Evol. 13:144-148(1999).

CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +

CC H(2)O.

CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing

CC the dimer (By similarity).

CC -1- PATHWAY: Glycolysis.

CC -1- SUBUNIT: Homodimer (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: Belongs to the enolase family.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

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CC removed.

CC -----

DR EMBL: AF072588; AAD41645.1; -, mRNA.

DR HSSP: P56252; 1PDZ.

DR SMR: Q9W7L1; 1-432.

DR InterPro: IPR000941; Enolase.

DR PANTHER: PTHR11902; Enolase; 1.

DR Pfam: PF00113; Enolase\_C; 1.

DR Pfam: PF03952; Enolase\_N; 1.

DR PRINTS: PR00148; ENOLASE.

DR ProDom: PD000902; Enolase; 1.

DR TIGRPFAM: TIGR01060; eno; 1.

DR PROSITE: PS00164; ENOLASE; 1.

KW Glycolysis; Lyase; Magnesium; Metal-binding; Multigene family.

FT INIT MET 0 0 By similarity.

FT METAL 244 244 Magnesium (By similarity).

FT METAL 292 292 Magnesium (By similarity).

FT METAL 317 317 Magnesium (By similarity).

SQ SEQUENCE 433 AA; 47202 MW; 08193329CA1D3006 CRC64;

Query Match 72.2%; Score 65; DB 1; Length 433;

Best Local Similarity 81.2%; Pred. No. 0.047;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16

DB 383 LVVGLCTGQIKTGAPC 398

ENOA\_TRASC STANDARD; PRT; 433 AA.

ID ENO7L1;

AC Q9W7L1;

DT 28-FEB-2003 (Rel. 41; Created)

DT 28-FEB-2003 (Rel. 41; Last sequence update)

DT 13-SEP-2005 (Rel. 48; Last annotation update)

DE Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)

OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Testudines; Cryptodira; Testudinoidae; Emydidae; Trachemys.

NCBI\_TaxId=34903;

RN (1)

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Subsp. elegans; TISSUE=Muscle;

RX MEDLINE=99439677; PubMed=10508547; DOI=10.1006/mpev.1999.0640;

RA Mannen H., Li S.S.-L.;

RT "Molecular evidence for a clade of turtles.";

RL Mol. Phylogenet. Evol. 13:144-148(1999).

CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +

CC H(2)O.

CC -1- COFACTOR: Magnesium. Required for catalysis and for stabilizing

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CC -1- PATHWAY: Glycolysis.

CC -1- SUBUNIT: Homodimer (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: Belongs to the enolase family.

CC -----

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CC removed.

CC -----

DR EMBL: AF072588; AAD41645.1; -, mRNA.

DR HSSP: P56252; 1PDZ.

DR SMR: Q9W7L1; 1-432.

DR InterPro: IPR000941; Enolase.

DR PANTHER: PTHR11902; Enolase; 1.

Search completed: April 3, 2006, 08:03:42

Job time : 59 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 08:03:55 ; Search time 21 Seconds  
(without alignments)  
62.991 Million cell updates/sec

Title: US-09-647-457E-3

Perfect score: 90

Sequence: 1 LVVGLCTCQIKTGPAK 16

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/prodata/1/1aa/5\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/6\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/H\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/RTUS\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/RB\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	72.2	434	2	US-09-949-016-6153
2	65	72.2	443	2	US-09-949-016-8359
3	46	51.1	45	1	US-07-973-852-1
4	46	51.1	45	1	US-07-950-773-1
5	46	51.1	46	2	US-09-030-619-230
6	46	51.1	46	2	US-09-444-281-111
7	45	50.0	712	2	US-09-252-991A-20471
8	43	47.8	100	2	US-10-105-901A-51
9	43	47.8	452	2	US-09-773-877B-16
10	43	47.8	462	2	US-09-773-877B-18
11	43	47.8	557	2	US-09-773-877B-14
12	43	47.8	567	2	US-09-773-877B-12
13	43	47.8	567	2	US-09-773-877B-20
14	43	47.8	661	1	US-08-232-538-12
15	43	47.8	661	1	US-08-786-164-12
16	43	47.8	687	1	US-08-232-538-6
17	43	47.8	687	1	US-08-786-164-6
18	43	47.8	687	2	US-09-427-353-2
19	43	47.8	758	1	US-08-874-678-1
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21	43	47.8	758	2	US-09-051-363-24
22	43	47.8	758	2	US-09-348-886-1
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24	43	47.8	780	1	US-08-232-538-14
25	43	47.8	780	1	US-08-786-164-14
26	43	47.8	911	2	US-09-949-002-425
27	43	47.8	1006	2	US-09-023-905A-12

28	43	47.8	1006	2	US-09-949-002-361	Sequence 361, App
29	43	47.8	1311	1	US-08-340-011-5	Sequence 5, Appl
30	43	47.8	1311	2	US-08-901-710-5	Sequence 5, Appl
31	43	47.8	1311	2	US-09-169-079-5	Sequence 5, Appl
32	43	47.8	1311	2	US-08-750-141A-3	Sequence 3, Appl
33	43	47.8	1338	2	US-08-874-678-33	Sequence 6, Appl
34	43	47.8	1362	1	US-08-119-014D-6	Sequence 33, Appl
35	43	47.8	1362	2	US-08-643-839-33	Sequence 33, Appl
36	43	47.8	1362	2	US-09-348-886-33	Sequence 33, Appl
37	43	47.8	1362	2	US-10-105-901A-33	Sequence 33, Appl
38	43	47.8	3542	2	US-10-087-013-2	Sequence 2, Appl
39	43	47.8	171	2	US-09-248-796A-21129	Sequence 21129, A
40	42	46.7	444	2	US-09-252-991A-21020	Sequence 21020, A
41	42	46.7	444	2	US-09-328-352-7269	Sequence 7269, Ap
42	42	46.7	445	2	US-09-540-236-2354	Sequence 2354, Ap
43	41.5	46.1	1101	2	US-09-561-709B-5	Sequence 5, Appl
44	41.5	46.1	1342	2	US-09-561-709B-13	Sequence 13, Appl
45	41.5	46.1	1761	2	US-09-561-709B-1	Sequence 1, Appl
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48	41	45.6	177	2	US-09-049-813-17	Sequence 17, Appl
49	41	45.6	177	2	US-09-227-853A-13	Sequence 13, Appl
50	41	45.6	178	1	US-08-465-794-18	Sequence 18, Appl
51	41	45.6	178	2	US-09-049-813-18	Sequence 18, Appl
52	41	45.6	178	2	US-08-663-191A-4	Sequence 4, Appl
53	40.5	45.0	2556	1	US-08-185-432-17	Sequence 17, Appl
54	40.5	45.0	2556	1	US-08-083-590A-20	Sequence 20, Appl
55	40.5	45.0	2556	2	US-08-532-384-20	Sequence 20, Appl
56	40.5	45.0	2556	2	US-08-899-232-2	Sequence 2, Appl
57	40.5	45.0	2556	2	US-09-121-457-2	Sequence 2, Appl
58	40.5	45.0	3084	2	US-09-562-702A-12	Sequence 12, Appl
59	40.5	45.0	3084	2	US-09-562-702A-10	Sequence 10, Appl
60	40	44.4	205	2	US-09-710-278-2510	Sequence 2510, Ap
61	40	44.4	300	2	US-09-198-452A-354	Sequence 354, App
62	40	44.4	341	2	US-09-438-185A-338	Sequence 338, App
63	40	44.4	476	2	US-09-252-991A-29179	Sequence 29179, A
64	40	44.4	891	2	US-09-134-001C-4913	Sequence 4913, Ap
65	40	44.4	2211	2	US-09-738-884-1	Sequence 1, Appl
66	40	44.4	2211	2	US-10-096-961A-4	Sequence 1, Appl
67	40	44.4	3307	2	US-10-029-217A-24	Sequence 24, Appl
68	39.5	43.9	1587	2	US-09-845-583A-10	Sequence 10, Appl
69	39.5	43.9	1587	2	US-09-561-709B-3	Sequence 3, Appl
70	39.5	43.9	2523	1	US-08-185-432-18	Sequence 18, Appl
71	39.5	43.9	2523	2	US-08-899-232-3	Sequence 3, Appl
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73	39	43.3	95	2	US-09-177-249-273	Sequence 273, App
74	39	43.3	115	2	US-09-812-283-273	Sequence 273, App
75	39	43.3	121	2	US-09-270-767-39953	Sequence 39953, A
76	39	43.3	121	2	US-09-270-767-39953	Sequence 39953, A
77	39	43.3	121	2	US-09-270-767-55170	Sequence 55170, A
78	39	43.3	160	2	US-09-248-796A-17879	Sequence 17879, A
79	39	43.3	180	2	US-09-510-238A-286	Sequence 286, App
80	39	43.3	272	2	US-09-270-767-34757	Sequence 34757, A
81	39	43.3	272	2	US-09-270-767-49974	Sequence 49974, A
82	39	43.3	384	2	US-09-945-249-8	Sequence 8, Appl
83	39	43.3	384	2	US-09-041-990-8	Sequence 8, Appl
84	39	43.3	481	1	US-07-927-071-1	Sequence 1, Appl
85	39	43.3	481	6	5164481-1	Patent No. 5164481
86	39	43.3	689	2	US-09-177-249-2	Sequence 2, Appl
87	39	43.3	689	2	US-09-061-268A-2	Sequence 2, Appl
88	39	43.3	689	2	US-09-812-783-2	Sequence 2, Appl
89	39	43.3	905	2	US-10-104-047-2128	Sequence 14, Appl
90	39	43.3	905	2	US-10-176-884-14	Sequence 1728, Ap
91	39	43.3	932	2	US-10-176-884-15	Sequence 15, Appl
92	39	43.3	992	1	US-08-127-499A-1	Sequence 1, Appl
93	39	43.3	992	1	US-08-482-847-1	Sequence 1, Appl
94	39	43.3	1063	1	US-08-093-453B-3	Sequence 3, Appl
95	39	43.3	1063	1	US-08-127-499A-8	Sequence 8, Appl
96	39	43.3	1063	1	US-08-482-847-8	Sequence 8, Appl
97	39	43.3	2353	2	US-08-984-709A-50	Sequence 50, Appl
98	39	43.3	2732	2	US-09-086-436-30	Sequence 30, Appl
99	38.5	42.8	65	6	5177197-51	Patent No. 5177197
100	38.5	42.8	410	6	5177197-1	Patent No. 5177197

## ALIGNMENTS

RESULT 1  
US-09-949-016-6153; Sequence 6153, Application US/09949016  
; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: C1001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6153

; LENGTH: 434

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-6153

Query Match 72.2%; Score 65; DB 2; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.16;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;QY 1 LVVGLCTCQIKTGAPC 16  
Db 384 LVVGLCTCQIKTGAPC 399

## RESULT 2

US-09-949-016-8359

; Sequence 8359, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: C1001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 8359

; LENGTH: 443

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-8359

Query Match 72.2%; Score 65; DB 2; Length 443;  
Best Local Similarity 81.2%; Pred. No. 0.16;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;QY 1 LVVGLCTCQIKTGAPC 16  
Db 393 LVVGLCTCQIKTGAPC 408RESULT 3  
US-07-973-852-1

; Sequence 1, Application US/07973852

; Patent No. 5376640

; GENERAL INFORMATION:

; APPLICANT: Miyazaki, Toshiyuki

; APPLICANT: Motoi, Hirofumi

; APPLICANT: Kodama, Toshiaki

; APPLICANT: Maeda, Tatsuhiro

; APPLICANT: Teujita, Takahiro

; TITLE OF INVENTION: LIPOLYTIC ENZYME INHIBITORS

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER &amp; NEUSTADT,

; ADDRESS: P.C.

; STREET: 1755 Jefferson Davis Highway, Fourth Floor

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/973,852

; FILING DATE:

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/631,321

; FILING DATE: 20-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 332884/1989

; FILING DATE: 25-DEC-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 75600/1990

; FILING DATE: 27-MAR-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 194782/1990

; FILING DATE: 25-JUL-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: OBLON, NO. 5376640man F.

; REGISTRATION NUMBER: 24,618

; REFERENCE/DOCKET NUMBER: 1327-014-0 DIV

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)521-4500

; TELEFAX: (703)486-2347

; TELEX: 248855 OPAT UR

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 45 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-07-973-852-1

Query Match 51.1%; Score 46; DB 1; Length 45;  
Best Local Similarity 43.8%; Pred. No. 8.8;  
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;QY 1 LVVGLCTCQIKTGAPC 16  
Db 24 LCAVCRCKISSGLSC 39

## RESULT 4

US-07-950-773-1

; Sequence 1, Application US/07950773

; Patent No. 5411956

; GENERAL INFORMATION:

; APPLICANT: Miyazaki, Toshiyuki

```

; APPLICANT: Motol, Hirofumi
; APPLICANT: Kodama, Toshiaki
; APPLICANT: Maeda, Tetsuro
; APPLICANT: Tsujita, Takahiro
; APPLICANT: Okuda, Hiromichi
; TITLE OF INVENTION: LIPOLYTIC ENZYME INHIBITORS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT, P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/950,773
; FILING DATE: 19920924
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/631,321
; FILING DATE: 20-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5411956man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1327-003-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-950-773-1

Query Match      51.1%; Score 46; DB 1; Length 45;
Best Local Similarity 43.8%; Pred. No. 8 8;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy      1 LVVGLCTCQIKTGPAK 16
Db      24 LCAGVCRCKISGSLGC 39

RESULT 5
US-09-030-619-230
; Sequence 230, Application US/09030619B
; Patent No. 6503881
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Brille, Douglas
; APPLICANT: Frazer, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 230
; LENGTH: 46
; TYPE: PRT

```

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; ORGANISM: Hordeum vulgare
; US-09-030-619-230

Query Match      51.1%; Score 46; DB 2; Length 46;
Best Local Similarity 53.8%; Pred. No. 9;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      4 GLCTCQIKTGPAK 16
Db      28 GACRCRKISGPKC 40

RESULT 6
US-09-444-281-111
; Sequence 111, Application US/09444281
; Patent No. 6946261
; GENERAL INFORMATION:
; APPLICANT: Burian, Jan
; APPLICANT: Bartfeld, Daniel
; TITLE OF INVENTION: EFFICIENT METHODS FOR PRODUCING
; FILE REFERENCE: 660081.411
; CURRENT APPLICATION NUMBER: US/09/444,281
; CURRENT FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Hordeum vulgare
; US-09-444-281-111

Query Match      51.1%; Score 46; DB 2; Length 46;
Best Local Similarity 53.8%; Pred. No. 9;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      4 GLCTCQIKTGPAK 16
Db      28 GACRCRKISGPKC 40

```

```

RESULT 7
US-09-252-991A-20471
; Sequence 20471, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20471
; LENGTH: 712
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-20471

Query Match      50.0%; Score 45; DB 2; Length 712;
Best Local Similarity 46.7%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy      2 VVGLCTCQIKTGPAK 16
Db      641 VTGSCRCNASSSPAC 655

RESULT 8

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```
US-10-105-901A-51
; Sequence 51, Application US/10105901A
; Patent No. 6897294
; GENERAL INFORMATION:
; APPLICANT: Davis-Smyth, Terri L.
; Chen, Helen H.
; Presta, Leonard
; Ferrara, Napoleone
; TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL
; GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR
; PRODUCTION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dorsney & Whitney LLP
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/105,901A
; FILING DATE: 20-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/348,886
; FILING DATE: 01-JUL-1999
; APPLICATION NUMBER: US 08/643,839
; FILING DATE: 07-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard F. Treacartin
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-63291-3/RFT/NBC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-10-105-901A-51

Query Match          47.8%; Score 43; DB 2; Length 100;
Best Local Similarity 50.0%; Pred. No. 47;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      4 GLCTCQIKTGPA 15
      |||:::|
Db      76 GLYTCRVRSGPS 87

RESULT 9
US-09-773-877B-16
; Sequence 16, Application US/09773877B
; Patent No. 6833349
; GENERAL INFORMATION:
; APPLICANT: Xia, Yu-Ping et al.
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
; FILE REFERENCE: REG 710B
; CURRENT APPLICATION NUMBER: US/09/773,877B
; CURRENT FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 16
.
```

```
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Flt1(2-3 deltab)-Fc
US-09-773-877B-16

Query Match          47.8%; Score 43; DB 2; Length 452;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      4 GLCTCQIKTGPA 15
      |||:::|
Db      192 GLYTCRVRSGPS 203

RESULT 10
US-09-773-877B-18
; Sequence 18, Application US/09773877B
; Patent No. 6833349
; GENERAL INFORMATION:
; APPLICANT: Xia, Yu-Ping et al.
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
; FILE REFERENCE: REG 710B
; CURRENT APPLICATION NUMBER: US/09/773,877B
; CURRENT FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 18
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Flt1(2-3)-Fc (Muc3)
US-09-773-877B-18

Query Match          47.8%; Score 43; DB 2; Length 462;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      4 GLCTCQIKTGPA 15
      |||:::|
Db      202 GLYTCRVRSGPS 213

RESULT 11
US-09-773-877B-14
; Sequence 14, Application US/09773877B
; Patent No. 6833349
; GENERAL INFORMATION:
; APPLICANT: Xia, Yu-Ping et al.
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
; FILE REFERENCE: REG 710B
; CURRENT APPLICATION NUMBER: US/09/773,877B
; CURRENT FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 14
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Flt1(1-3 deltab)-Fc (Muc1)
US-09-773-877B-14

Query Match          47.8%; Score 43; DB 2; Length 557;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      4 GLCTCQIKTGPA 15
      |||:::|
Db      297 GLYTCRVRSGPS 308
```



RESULT 12  
US-09-773-877B-12  
Sequence 12, Application US/09773877B  
Patent No. 6833349  
GENERAL INFORMATION:  
APPLICANT: Xia, Yu-Ping et al.  
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
FILE REFERENCE: REG 710B  
CURRENT APPLICATION NUMBER: US/09/773,877B  
CURRENT FILING DATE: 2001-01-31  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 12  
LENGTH: 567  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Flc(1-3)-Fc  
US-09-773-877B-12

Query Match 47.8%; Score 43; DB 2; Length 567;  
Best Local Similarity 50.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 4 GLCTCOIKTGP 15  
DB 307 GLYTCRVSGPS 318

RESULT 13  
US-09-773-877B-20  
Sequence 20, Application US/09773877B  
Patent No. 6833349  
GENERAL INFORMATION:  
APPLICANT: Xia, Yu-Ping et al.  
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
FILE REFERENCE: REG 710B  
CURRENT APPLICATION NUMBER: US/09/773,877B  
CURRENT FILING DATE: 2001-01-31  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 20  
LENGTH: 567  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Flc(1-3 R->N)-Fc (Mut4)  
US-09-773-877B-20

Query Match 47.8%; Score 43; DB 2; Length 567;  
Best Local Similarity 50.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 4 GLCTCOIKTGP 15  
DB 307 GLYTCRVSGPS 318

RESULT 14  
US-08-233-538-12  
Sequence 12, Application US/08232538  
Patent No. 5712380  
GENERAL INFORMATION:  
APPLICANT: Thomas, Kenneth A.  
APPLICANT: Kendall, Richard L.  
TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL CELL  
TITLE OF INVENTION: GROWTH FACTOR  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000 126 E Lincoln Avenue  
CITY: Rahway

STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,538  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Mallen, John W. III  
REGISTRATION NUMBER: 35,403  
REFERENCE/DOCKET NUMBER: 188881A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-3905  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 661 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-232-538-12

Query Match 47.8%; Score 43; DB 1; Length 661;  
Best Local Similarity 50.0%; Pred. No. 2.6e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 4 GLCTCOIKTGP 15  
DB 281 GLYTCRVSGPS 292

RESULT 15  
US-08-786-164-12  
Sequence 12, Application US/08786164  
Patent No. 5861484  
GENERAL INFORMATION:  
APPLICANT: THOMAS, KENNETH A.  
APPLICANT: KENDALL, RICHARD L.  
TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL  
TITLE OF INVENTION: CELL GROWTH FACTOR  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/786,164  
FILING DATE: 21-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark Hard, J  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 18888DA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-594-3905  
TELEFAX: 908-594-4720

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TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 661 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-786-164-12

Query Match
Best Local Similarity 47.8%; Score 43; DB 1; Length 661;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GLCTCQIKTGPA 15
Db 281 GLYTCRVRSGPS 292

RESULT 16
US-08-232-538-6
; Sequence 6, Application US/08232538
; Patent No. 5712380
; GENERAL INFORMATION:
; APPLICANT: Thomas, Kenneth A.
; APPLICANT: Kendall, Richard L.
; TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL CELL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232.538
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Wallen, John W.III
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: 188881A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 687 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-232-538-6

Query Match
Best Local Similarity 47.8%; Score 43; DB 1; Length 687;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GLCTCQIKTGPA 15
Db 307 GLYTCRVRSGPS 318

RESULT 17
US-08-786-164-6
; Sequence 6, Application US/08786164
```

```
; Patent No. 5861484
; GENERAL INFORMATION:
; APPLICANT: THOMAS, KENNETH A.
; APPLICANT: Kendall, Richard L.
; TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: CELL GROWTH FACTOR
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/786,164
; FILING DATE: 21-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark Hand, J
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18888DA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3905
; TELEFAX: 908-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 687 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-786-164-6

Query Match
Best Local Similarity 47.8%; Score 43; DB 1; Length 687;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GLCTCQIKTGPA 15
Db 307 GLYTCRVRSGPS 318

RESULT 18
US-09-427-353-2
; Sequence 2, Application US/09427353
; Patent No. 6375929
; GENERAL INFORMATION:
; APPLICANT: THOMAS, KENNETH A.
; APPLICANT: GOLDMAN, COREY K.
; APPLICANT: Kendall, Richard L.
; APPLICANT: BETT, ANDREW J.
; APPLICANT: HUCKLE, WILLIAM R.
; TITLE OF INVENTION: GENE THERAPY FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/427,353  
CLASSIFICATION:  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: HAND, MARK  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 19810YCA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-3905  
TELEFAX: 732-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 687 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE:  
US-09-427-353-2

Query Match 47.8%; Score 43; DB 2; Length 687;  
Best Local Similarity 50.0%; Pred. No. 2.7e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
Qy 4 GLTCTQIKTQPA 15  
Db 307 GLYTCRVRSGPS 318

RESULT 19  
US-08-874-678-1  
Sequence 1, Application US/08874678  
Patent No. 5952199  
GENERAL INFORMATION:  
APPLICANT: Davis-Smyth, Terri L.  
APPLICANT: Chen, Helen H.  
APPLICANT: Presta, Leonard  
APPLICANT: Ferrara, Napoleone  
TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL GROWTH FACTOR  
TITLE OF INVENTION: ACTIVITY, THEIR USES AND PROCESSES FOR THEIR PRODUCTION  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/874,678  
FILING DATE: HEREWITH  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/643,839  
FILING DATE: 07-MAY-1996  
ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.  
REGISTRATION NUMBER: 24,190  
REFERENCE/DOCKET NUMBER: A-63291-1/WHD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 758 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-874-678-1

Query Match 47.8%; Score 43; DB 1; Length 758;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
Qy 4 GLTCTQIKTQPA 15  
Db 307 GLYTCRVRSGPS 318

RESULT 20  
US-08-643-839-1  
Sequence 1, Application US/08643839  
Patent No. 6100071  
GENERAL INFORMATION:  
APPLICANT: Davis-Smyth, Terri L.  
APPLICANT: Chen, Helen H.  
APPLICANT: Presta, Leonard  
APPLICANT: Ferrara, Napoleone  
TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL  
TITLE OF INVENTION: GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/643,839  
FILING DATE: 07-MAY-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Walter H.  
REGISTRATION NUMBER: 24,190  
REFERENCE/DOCKET NUMBER: A-63291/WHD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 758 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-643-839-1

Query Match 47.8%; Score 43; DB 2; Length 758;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;

Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGA 15  
DB 307 GLYTCRVRSGPS 318

RESULT 21  
US-09-051-363-24  
; Sequence 24, Application US/09051363  
; Patent No. 6270993  
; GENERAL INFORMATION:  
; APPLICANT: Shibuya, Masabumi  
; APPLICANT: Okamoto, Masaaji  
; APPLICANT: Niwa, Mikio  
; APPLICANT: Matsumoto, Tomoe  
; APPLICANT: Asano, Makoto  
; APPLICANT: Segawa, Toshiaki  
; TITLE OF INVENTION: VEGF-BINDING POLYPEPTIDES  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/051.363  
; FILING DATE: 07-APR-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP96/02906  
; FILING DATE: 07-OCT-1996  
; APPLICATION NUMBER: 8/211892 JP  
; FILING DATE: 23-JUL-1996  
; APPLICATION NUMBER: 7/296476 JP  
; FILING DATE: 07-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fraser, Ph.D., J.D., Janis K.  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 06501/012001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 758 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-09-051-363-24

Query Match 47.8%; Score 43; DB 2; Length 758;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGA 15  
DB 307 GLYTCRVRSGPS 318

RESULT 22  
US-09-348-886-1  
; Sequence 1, Application US/09348886  
; Patent No. 638486  
; GENERAL INFORMATION:

; APPLICANT: Davis-Smyth, Terri L.  
; APPLICANT: Chen, Helen H.  
; APPLICANT: Presta, Leonard  
; APPLICANT: Ferrara, Napoleone  
; TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL  
; TITLE OF INVENTION: GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/348,886  
; FILING DATE: 01-JUL-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/643,839  
; FILING DATE: 07-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dolly A. Vance  
; REGISTRATION NUMBER: 39,054  
; REFERENCE/DOCKET NUMBER: A-63291-2/RMS/DAV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 758 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-09-348-886-1

Query Match 47.8%; Score 43; DB 2; Length 758;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGA 15  
DB 307 GLYTCRVRSGPS 318

RESULT 23  
US-10-105-901A-1  
; Sequence 1, Application US/10105901A  
; Patent No. 6897294  
; GENERAL INFORMATION:  
; APPLICANT: Davis-Smyth, Terri L.  
; APPLICANT: Chen, Helen H.  
; APPLICANT: Presta, Leonard  
; APPLICANT: Ferrara, Napoleone  
; TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL  
; TITLE OF INVENTION: GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR  
; PRODUCTION  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dorsey & Whitney LLP  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/105,901A  
FILING DATE: 20-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/348,886  
FILING DATE: 01-JUL-1999  
APPLICATION NUMBER: US 08/643,839  
FILING DATE: 07-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Richard F. Treccatlin  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-63291-3/RFT/NBC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 758 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-105-901A-1

Query Match 47.8%; Score 43; DB 2; Length 758;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGP 15  
DB 307 GLYTCRVRSGPS 318

RESULT 24  
US-08-232-538-14  
Sequence 14, Application US/08232538  
Patent No. 5712380  
GENERAL INFORMATION:  
APPLICANT: Thomas, Kenneth A.  
APPLICANT: Kendall, Richard L.  
TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL CELL  
TITLE OF INVENTION: GROWTH FACTOR  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000 126 E Lincoln Avenue  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,538  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Wallen, John W.III  
REGISTRATION NUMBER: 35,403  
REFERENCE/DOCKET NUMBER: 188881A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-3905

TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 780 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-232-538-14

Query Match 47.8%; Score 43; DB 1; Length 780;  
Best Local Similarity 50.0%; Pred. No. 3e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGP 15  
DB 307 GLYTCRVRSGPS 318

RESULT 25  
US-08-786-164-14  
Sequence 14, Application US/08786164  
Patent No. 5861484  
GENERAL INFORMATION:  
APPLICANT: THOMAS, KENNETH A.  
APPLICANT: KENDALL, RICHARD L.  
TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL  
TITLE OF INVENTION: CELL GROWTH FACTOR  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/786,164  
FILING DATE: 21-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark Hard, J  
REGISTRATION NUMBER: 36,545  
REFERENCE/DOCKET NUMBER: 18888DA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-594-3905  
TELEFAX: 908-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 780 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-786-164-14

Query Match 47.8%; Score 43; DB 1; Length 780;  
Best Local Similarity 50.0%; Pred. No. 3e+02;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGP 15  
DB 307 GLYTCRVRSGPS 318

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RESULT 26
US-09-949-002-425
; Sequence 425, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 425
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-425

Query Match          47.8%; Score 43; DB 2; Length 911;
Best Local Similarity 58.3%; Pred. No. 3.4e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 VGLCTCQIKTGP 14
: |||||
Db 365 LNLITCQVKTNP 376

RESULT 27
US-09-023-905A-12
; Sequence 12, Application US/09023905A
; Patent No. 6475778
; GENERAL INFORMATION:
; APPLICANT: Roberts, Thomas M.
; APPLICANT: King, Frederick J.
; APPLICANT: Harris, David F.
; APPLICANT: Hu, Erding
; APPLICANT: Spiegelman, Bruce
; APPLICANT: Chan, Joanne
; TITLE OF INVENTION: Differentiation Enhancing Factors and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: DFN-021
; CURRENT APPLICATION NUMBER: US/09/023,905A
; CURRENT FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/038,191
; PRIOR FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1006
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-023-905A-12

Query Match          47.8%; Score 43; DB 2; Length 1006;
Best Local Similarity 58.3%; Pred. No. 3.8e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 VGLCTCQIKTGP 14
: |||||
Db 349 LNLITCQVKTNP 360

RESULT 28
US-09-949-002-361
; Sequence 361, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 361
; LENGTH: 1006
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-361

Query Match          47.8%; Score 43; DB 2; Length 1006;
Best Local Similarity 58.3%; Pred. No. 3.8e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 VGLCTCQIKTGP 14
: |||||
Db 349 LNLITCQVKTNP 360

RESULT 29
US-08-340-011-5
; Sequence 5, Application US/08340011
; Patent No. 5776755
; GENERAL INFORMATION:
; APPLICANT: Altalo, et al.
; TITLE OF INVENTION: FLT4, A NOVEL RECEPTOR TYROSIN KINASE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,011
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959,951
; FILING DATE: 09-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: 32267
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1311 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-340-011-5

Query Match          47.8%; Score 43; DB 1; Length 1311;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
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OY 4 GLCTCQIKTGPA 15  
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 DB 317 GLYTCRVRSGPS 328

RESULT 30

US-08-901-710-5  
 ; Sequence 5, Application US/08901710  
 ; Patent No. 6107046  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alitalo, Kari  
 ; APPLICANT: Apalikova, Olga  
 ; APPLICANT: Pajusola, Katri  
 ; APPLICANT: Armstrong, Elna  
 ; APPLICANT: Korhonen, Jaana  
 ; APPLICANT: Kaipainen, Arja  
 ; APPLICANT: Mälikäinen, Marja-Terttu  
 ; TITLE OF INVENTION: FLT4, A RECEPTOR TYROSINE KINASE, AND USES  
 ; TITLE OF INVENTION: THEREOF  
 ; NUMBER OF SEQUENCES: 20  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: United States of America  
 ; ZIP: 60606-6402  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/901,710  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/340,011  
 ; FILING DATE: 14-NOV-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/257,754  
 ; FILING DATE: 09-JUL-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/959,951  
 ; FILING DATE: 09-OCT-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Gass, David A.  
 ; REGISTRATION NUMBER: 38,153  
 ; REFERENCE/DOCKET NUMBER: 28113/33824  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 312/474-6300  
 ; TELEFAX: 312/474-0448  
 ; TELEX: 25-3856  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1311 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-901-710-5

Query Match 47.8%; Score 43; DB 2; Length 1311;  
 Best Local Similarity 50.0%; Pred. No. 4.8e+02;  
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 4 GLCTCQIKTGPA 15  
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 DB 317 GLYTCRVRSGPS 328

Search completed: April 3, 2006, 08:04:25  
 Job time : 23 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 3, 2006, 08:04:51 ; Search time 166 Seconds  
(without alignments)  
40.273 Million cell updates/sec

Title: US-09-647-457F-3  
Perfect score: 90  
Sequence: 1 LVWGLCTCQIKTGAPAC 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

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2: /cgn2\_6/ptodata/1/pubppaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubppaa/US10\_PUBCOMB.pep:\*  
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6: /cgn2\_6/ptodata/1/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	82.2	458	5	US-10-733-969A-13
2	74	82.2	458	5	US-10-478-519-6
3	65	72.2	50	5	US-10-776-013-325
4	65	72.2	269	5	US-10-473-127-1043
5	65	72.2	272	5	US-10-473-127-1041
6	65	72.2	272	5	US-10-473-127-1041
7	65	72.2	336	5	US-10-473-127-1042
8	65	72.2	420	5	US-10-498-788-17
9	65	72.2	429	5	US-10-473-127-604
10	65	72.2	433	3	US-09-935-642-9
11	65	72.2	433	5	US-10-733-969A-61
12	65	72.2	433	5	US-10-473-127-608
13	65	72.2	433	5	US-10-473-127-610
14	65	72.2	434	4	US-10-177-293-124
15	65	72.2	434	4	US-10-205-194-47
16	65	72.2	434	4	US-10-354-358-16
17	65	72.2	434	4	US-10-170-385-257
18	65	72.2	434	4	US-10-170-385-273
19	65	72.2	434	4	US-10-258-666-10
20	65	72.2	434	4	US-10-205-331-26
21	65	72.2	434	5	US-10-473-127-595
22	65	72.2	434	5	US-10-473-127-596
23	65	72.2	434	5	US-10-473-127-597
24	65	72.2	434	5	US-10-473-127-598
25	65	72.2	434	5	US-10-473-127-599
26	65	72.2	434	5	US-10-473-127-600
27	65	72.2	434	5	US-10-473-127-601

28	65	72.2	434	5	US-10-473-127-602	Sequence 602, App
29	65	72.2	434	5	US-10-473-127-603	Sequence 603, App
30	65	72.2	434	5	US-10-473-127-609	Sequence 609, App
31	65	72.2	434	5	US-10-723-860-1117	Sequence 1717, App
32	65	72.2	434	5	US-10-723-860-1948	Sequence 1948, App
33	65	72.2	434	5	US-10-370-715B-38	Sequence 38, App
34	65	72.2	434	5	US-10-873-595-15	Sequence 15, App
35	65	72.2	434	5	US-10-489-740-146	Sequence 146, App
36	65	72.2	434	5	US-10-491-548A-36	Sequence 36, App
37	65	72.2	434	5	US-10-676-691-13	Sequence 13, App
38	65	72.2	434	5	US-10-676-691-15	Sequence 15, App
39	65	72.2	434	5	US-10-676-691-21	Sequence 21, App
40	65	72.2	434	5	US-10-676-691-22	Sequence 22, App
41	65	72.2	434	5	US-10-676-691-23	Sequence 23, App
42	65	72.2	434	5	US-10-287-436A-373	Sequence 373, App
43	65	72.2	434	5	US-10-287-436A-1074	Sequence 1074, App
44	59	62.2	434	5	US-10-676-691-24	Sequence 24, App
45	56	62.2	163	4	US-10-767-701-55929	Sequence 55929, App
46	56	62.2	434	4	US-10-369-493-5507	Sequence 5507, App
47	55	61.1	433	6	US-11-097-143-30645	Sequence 30645, App
48	52	57.8	112	4	US-10-437-963-192587	Sequence 192587, App
49	52	57.8	200	4	US-10-437-963-192579	Sequence 192579, App
50	52	57.8	372	4	US-10-437-963-192575	Sequence 192575, App
51	52	57.8	449	4	US-10-437-963-192589	Sequence 192589, App
52	51	56.7	66	3	US-09-864-408A-6276	Sequence 6276, App
53	51	56.7	103	4	US-10-437-963-192583	Sequence 192583, App
54	51	56.7	211	4	US-10-425-114-57843	Sequence 57843, App
55	51	56.7	245	4	US-10-425-114-46733	Sequence 46733, App
56	51	56.7	292	4	US-10-437-963-144071	Sequence 144071, App
57	51	56.7	447	4	US-10-425-115-212253	Sequence 212253, App
58	50	55.6	93	4	US-10-425-115-264306	Sequence 264306, App
59	50	55.6	80	4	US-10-425-114-48757	Sequence 48757, App
60	50	55.6	152	4	US-10-425-114-56560	Sequence 56560, App
61	50	55.6	226	4	US-10-425-114-48844	Sequence 48844, App
62	50	55.6	284	4	US-10-424-599-156709	Sequence 156709, App
63	50	55.6	286	4	US-10-424-599-156701	Sequence 156701, App
64	50	55.6	287	4	US-10-424-599-156701	Sequence 156701, App
65	50	55.6	411	4	US-10-425-115-47263	Sequence 47263, App
66	50	55.6	444	4	US-10-425-115-261716	Sequence 261716, App
67	50	55.6	447	4	US-10-424-599-261184	Sequence 261184, App
68	50	55.6	449	4	US-10-369-493-3639	Sequence 3639, App
69	49	54.4	164	4	US-10-425-114-64646	Sequence 64646, App
70	49	54.4	177	4	US-10-425-114-46609	Sequence 46609, App
71	49	54.4	220	4	US-10-425-114-51600	Sequence 51600, App
72	49	54.4	260	4	US-10-425-114-68956	Sequence 68956, App
73	49	54.4	284	4	US-10-425-115-258706	Sequence 258706, App
74	48	53.3	94	4	US-10-425-114-45521	Sequence 45521, App
75	48	53.3	110	4	US-10-425-115-207365	Sequence 207365, App
76	48	53.3	113	4	US-10-767-701-57224	Sequence 57224, App
77	48	53.3	201	4	US-10-425-114-43256	Sequence 43256, App
78	48	53.3	403	4	US-10-437-963-111671	Sequence 111671, App
79	48	53.3	476	5	US-10-739-990-8212	Sequence 8212, App
80	48	53.3	512	4	US-10-425-114-43444	Sequence 43444, App
81	48	53.3	529	4	US-10-425-115-207376	Sequence 207376, App
82	48	53.3	2037	4	US-10-184-664-591	Sequence 591, App
83	48	53.3	2037	4	US-10-184-664-591	Sequence 591, App
84	48	53.3	2542	4	US-10-123-155-95	Sequence 95, App
85	48	53.3	2542	4	US-10-146-721-95	Sequence 95, App
86	48	53.3	2542	4	US-10-146-721-95	Sequence 95, App
87	48	53.3	2542	4	US-10-141-761-95	Sequence 95, App
88	48	53.3	2542	4	US-10-141-761-95	Sequence 95, App
89	48	53.3	2542	4	US-10-142-885-95	Sequence 95, App
90	48	53.3	2542	4	US-10-158-790-95	Sequence 95, App
91	48	53.3	2542	4	US-10-137-871-95	Sequence 95, App
92	48	53.3	2542	4	US-10-140-923-95	Sequence 95, App
93	48	53.3	2542	4	US-10-141-756-95	Sequence 95, App
94	48	53.3	2542	4	US-10-141-759-95	Sequence 95, App
95	48	53.3	2542	4	US-10-140-805-95	Sequence 95, App
96	48	53.3	2542	4	US-10-140-864-95	Sequence 95, App
97	48	53.3	4277	4	US-10-184-644-439	Sequence 439, App
98	47	52.2	59	4	US-10-184-634-439	Sequence 439, App
99	47	52.2	166	4	US-10-425-115-259324	Sequence 259324, App
100	46.5	51.7	437	4	US-10-369-493-22001	Sequence 22001, App

## ALIGNMENTS

RESULT 1

```
US-10-733-969A-13
; Sequence 13, Application US/10733969A
; Publication No. US20040219572A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, JIE
; APPLICANT: HU, LIPING
; APPLICANT: LIU, TONG HUA
; APPLICANT: LU, ZHAO HUI
; APPLICANT: SHEN, YAN
; TITLE OF INVENTION: SPECIFIC MARKERS FOR PANCREATIC CANCER
; FILE REFERENCE: 21525
; CURRENT APPLICATION NUMBER: US/10/733, 969A
; CURRENT FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: EP 02028058.2
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Alpha enolase; Accession NO: aa of 06 Dec 2002: Q05524
US-10-733-969A-13
```

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Query Match      82.2%; Score 74; DB 5; Length 458;
Best Local Similarity 87.5%; Pred. No. 0.023;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 1 LVVGLCTCQIKTGTPAC 16

Db 407 LVVGLCTGQIKTGPTC 422

RESULT 2

```
US-10-478-519-6
; Sequence 6, Application US/10478519
; Publication No. US20050042738A1
; GENERAL INFORMATION:
; APPLICANT: SMARNAKAR, Anita; GORVAD, Ann E.;
; APPLICANT: HAPALIA, April J.A.; DUGGAN, Brendan M.;
; APPLICANT: EMERLING, Brooke M.; ISON, Craig H.;
; APPLICANT: NGUYEN, Daniel B.; LEE, Ernestine A.;
; APPLICANT: YUE, Henry; YUE, Hubin;
; APPLICANT: FORSYTHE, Ian J.; LI, Joana X.;
; APPLICANT: THANGAVELU, Kavitha; CHAMLA, Narinder K.;
; APPLICANT: BURFORD, Neil; MASON, Patricia M.;
; APPLICANT: LAL, Preeti G.; LEE, Sally;
; APPLICANT: BECHA, Shanya D.; TANG, Y. Tom
; TITLE OF INVENTION: Carbohydrate-Associated Proteins
; FILE REFERENCE: EP-0982 USN
; CURRENT APPLICATION NUMBER: US/10/478, 519
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/US02/18354
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/293, 768
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/309, 548
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 60/314, 400
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US 60/343, 706
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/337, 999
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
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; SEQ ID NO 6

; LENGTH: 458

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No: 7488348CD1

US-10-478-519-6

```
Query Match      82.2%; Score 74; DB 5; Length 458;
Best Local Similarity 87.5%; Pred. No. 0.023;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 1 LVVGLCTCQIKTGTPAC 16

Db 407 LVVGLCTGQIKTGPTC 422

RESULT 3

```
US-10-776-013-325
; Sequence 325, Application US/10776013
; Publication No. US20040226056A1
; GENERAL INFORMATION:
; APPLICANT: MYRIAD GENETICS, INC.
; APPLICANT: ROCH, Jean-Marc
; APPLICANT: BARTHEL, Paul
; APPLICANT: HEICHMAN, Karen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEUROLOGICAL DISORDERS AND
; FILE REFERENCE: 1600.24
; CURRENT APPLICATION NUMBER: US/10/776, 013
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 09/948904
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 09/466139
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/113534
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/124120
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/141243
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/975072
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 10/194967
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 60/304775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 695
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 325
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-776-013-325
```

```
Query Match      72.2%; Score 65; DB 5; Length 50;
Best Local Similarity 81.2%; Pred. No. 0.058;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

QY 1 LVVGLCTCQIKTGTPAC 16

Db 24 LVVGLCTGQIKTGAPC 39

RESULT 4

```
US-10-473-127-1043
; Sequence 1043, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: ZYCOS Inc.
```

```

; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1043
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1043
```

```
Query Match          72.2%; Score 65; DB 5; Length 269;
Best Local Similarity 81.2%; Pred. No. 0.26;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      1 LVVGLCTGQIKTGAPC 16
Db      219 LVVGLCTGQIKTGAPC 234
```

```

RESULT 5
US-10-473-127-1041
; Sequence 1041, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1041
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1041
```

```
Query Match          72.2%; Score 65; DB 5; Length 272;
Best Local Similarity 81.2%; Pred. No. 0.27;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      1 LVVGLCTGQIKTGAPC 16
Db      222 LVVGLCTGQIKTGAPC 237
```

RESULT 6

```

US-10-473-127-1044
; Sequence 1044, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1044
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1044
```

```
Query Match          72.2%; Score 65; DB 5; Length 272;
Best Local Similarity 81.2%; Pred. No. 0.27;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      1 LVVGLCTGQIKTGAPC 16
Db      222 LVVGLCTGQIKTGAPC 237
```

```

RESULT 7
US-10-473-127-1042
; Sequence 1042, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1042
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1042
```

```
Query Match          72.2%; Score 65; DB 5; Length 336;
Best Local Similarity 81.2%; Pred. No. 0.32;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      1 LVVGLCTGQIKTGAPC 16
```

Db 286 LVVGLCTGQIKTGAPC 301

## RESULT 8

US-10-498-788-17  
; Sequence 17, Application US/10498788  
; Publication No. US20050118594A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: Chawla, Nandinder K.  
; APPLICANT: Lee, Soo Yeun  
; APPLICANT: Ring, Huijun Z.  
; APPLICANT: Lee, Ernestine A.  
; APPLICANT: Foreythe, Ian J.  
; APPLICANT: Khare, Reena  
; APPLICANT: Tran, Uyen K.  
; APPLICANT: Kable, Amy E.  
; APPLICANT: Richardson, Thomas W.  
; APPLICANT: Emerling, Brooke M.  
; APPLICANT: Lindquist, Erika A.  
; APPLICANT: Baughn, Mariah R.  
; APPLICANT: Hafalia, April J. A.  
; APPLICANT: Jin, Pei  
; APPLICANT: Swarnakar, Anita  
; APPLICANT: Li, Joana X.  
; APPLICANT: Marquis, Joseph P.  
; APPLICANT: Lee, Sally  
; APPLICANT: Gorvad, Ann F.  
; APPLICANT: Sprague, William W.  
; APPLICANT: Bedna, Shanya D.  
; APPLICANT: Elliott, Vicki S.  
; TITLE OF INVENTION: ENZYMES  
; FILE REFERENCE: PF-1312 PCT  
; CURRENT APPLICATION NUMBER: US/10/498,788  
; CURRENT FILING DATE: 2004-06-14  
; PRIOR APPLICATION NUMBER: US 60/340,357  
; PRIOR FILING DATE: 2001-12-14  
; PRIOR APPLICATION NUMBER: US 60/342,962  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: US 60/343,558  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: US 60/351,107  
; PRIOR FILING DATE: 2002-01-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: PERL Program  
; SEQ ID NO 17  
; LENGTH: 420  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: incyte ID No: 7506054CD1  
US-10-498-788-17

Query Match 72.2%; Score 65; DB 5; Length 420;  
Best Local Similarity 81.2%; Pred. No. 0.39;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
Db 370 LVVGLCTGQIKTGAPC 385

## RESULT 9

US-10-473-127-604  
; Sequence 604, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026WO1  
; CURRENT APPLICATION NUMBER: US/10/473,127

; CURRENT FILING DATE: 2003-09-26

; PRIOR APPLICATION NUMBER: 60/279,495

; PRIOR FILING DATE: 2001-03-28

; PRIOR APPLICATION NUMBER: 60/292,544

; PRIOR FILING DATE: 2001-05-21

; PRIOR APPLICATION NUMBER: 60/310,801

; PRIOR FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: 60/326,370

; PRIOR FILING DATE: 2001-10-01

; PRIOR APPLICATION NUMBER: 60/336,780

; PRIOR FILING DATE: 2001-12-04

; PRIOR APPLICATION NUMBER: 60/358,985

; PRIOR FILING DATE: 2002-02-20

; NUMBER OF SEQ ID NOS: 2041

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 604

; LENGTH: 429

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-473-127-604

Query Match 72.2%; Score 65; DB 5; Length 429;  
Best Local Similarity 81.2%; Pred. No. 0.4;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
Db 379 LVVGLCTGQIKTGAPC 394

## RESULT 10

US-09-935-642-9  
; Sequence 9, Application US/09935642  
; Publication No. US20030044795A1  
; GENERAL INFORMATION:  
; APPLICANT: BYRJALSEN, Inger  
; APPLICANT: LARSEN, Peter  
; APPLICANT: STEPHEN, John  
; TITLE OF INVENTION: Biochemical Markers for the Human  
; FILE REFERENCE: 8969-014  
; CURRENT APPLICATION NUMBER: US/09/935,642  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: PCT/GB97/02394  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: PCT/GB9707132.8  
; PRIOR FILING DATE: 1997-04-08  
; PRIOR APPLICATION NUMBER: PCT/GB9618600.2  
; PRIOR FILING DATE: 1996-09-06  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 433  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-642-9

Query Match 72.2%; Score 65; DB 3; Length 433;  
Best Local Similarity 81.2%; Pred. No. 0.41;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
Db 383 LVVGLCTGQIKTGAPC 398

## RESULT 11

US-10-733-969A-61  
; Sequence 61, Application US/10733969A  
; Publication No. US20040219572A1  
; GENERAL INFORMATION:  
; APPLICANT: CHEN, JIE  
; APPLICANT: HU, LIPING

APPLICANT: LIU, TONG HUA  
APPLICANT: LU, ZHAO HUI  
APPLICANT: SHEN, YAN  
TITLE OF INVENTION: SPECIFIC MARKERS FOR PANCREATIC CANCER  
FILE REFERENCE: 21525  
CURRENT APPLICATION NUMBER: US/10/733,969A  
CURRENT FILING DATE: 2003-12-11  
PRIOR APPLICATION NUMBER: EP 02028058.2  
PRIOR FILING DATE: 2002-12-17  
NUMBER OF SEQ ID NOS: 110  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 61  
LENGTH: 433  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: human alpha enolase; Accession NO:  
US-10-733-969A-61

Query Match 72.2%; Score 65; DB 5; Length 433;  
Best Local Similarity 81.2%; Pred. No. 0.41;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 383 LVVGLCTGQIKTGAPC 398

RESULT 12  
US-10-473-127-608  
Sequence 608, Application US/10473127  
Publication No. US20040236091A1  
GENERAL INFORMATION:  
APPLICANT: Zycos Inc.  
TITLE OF INVENTION: TRANSLATIONAL PROFILING  
FILE REFERENCE: 08191-026W01  
CURRENT APPLICATION NUMBER: US/10/473,127  
CURRENT FILING DATE: 2003-09-26  
PRIOR APPLICATION NUMBER: 60/279,495  
PRIOR FILING DATE: 2001-03-28  
PRIOR APPLICATION NUMBER: 60/292,544  
PRIOR FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: 60/310,801  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: 60/326,370  
PRIOR FILING DATE: 2001-10-01  
PRIOR APPLICATION NUMBER: 60/336,780  
PRIOR FILING DATE: 2001-12-04  
PRIOR APPLICATION NUMBER: 60/358,985  
PRIOR FILING DATE: 2002-02-20  
NUMBER OF SEQ ID NOS: 2041  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 608  
LENGTH: 433  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-473-127-608

Query Match 72.2%; Score 65; DB 5; Length 433;  
Best Local Similarity 81.2%; Pred. No. 0.41;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 383 LVVGLCTGQIKTGAPC 398

RESULT 13  
US-10-473-127-610  
Sequence 610, Application US/10473127  
Publication No. US20040236091A1  
GENERAL INFORMATION:

APPLICANT: Zycos Inc.  
TITLE OF INVENTION: TRANSLATIONAL PROFILING  
FILE REFERENCE: 08191-026W01  
CURRENT APPLICATION NUMBER: US/10/473,127  
CURRENT FILING DATE: 2003-09-26  
PRIOR APPLICATION NUMBER: 60/279,495  
PRIOR FILING DATE: 2001-03-28  
PRIOR APPLICATION NUMBER: 60/292,544  
PRIOR FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: 60/310,801  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: 60/326,370  
PRIOR FILING DATE: 2001-10-01  
PRIOR APPLICATION NUMBER: 60/336,780  
PRIOR FILING DATE: 2001-12-04  
PRIOR APPLICATION NUMBER: 60/358,985  
PRIOR FILING DATE: 2002-02-20  
NUMBER OF SEQ ID NOS: 2041  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 610  
LENGTH: 433  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-473-127-610

Query Match 72.2%; Score 65; DB 5; Length 433;  
Best Local Similarity 81.2%; Pred. No. 0.41;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 383 LVVGLCTGQIKTGAPC 398

RESULT 14  
US-10-177-293-124  
Sequence 124, Application US/10177293  
Publication No. US20030124128A1  
GENERAL INFORMATION:  
APPLICANT: Lilly, James  
APPLICANT: Glatc, Karen  
APPLICANT: Zhao, Xumei  
APPLICANT: Ganavarpur Manjula  
APPLICANT: Kametkar, Shubhangi  
APPLICANT: Mertens, Maureen  
APPLICANT: Myer, Vlc  
APPLICANT: Wang, Youzhen  
APPLICANT: Xu, Yongyao  
APPLICANT: Hoersch, Sebastian  
APPLICANT: Monahan, John  
APPLICANT: Meyers, Rachel E.  
APPLICANT: Baat Jr., Robert C.  
APPLICANT: Horobagyl, Gabriel N.  
APPLICANT: Pusztai, Lajos  
APPLICANT: Meric, Funda  
APPLICANT: Sahin, Aysegul  
APPLICANT: Mills, Gordon B.  
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,  
PREVENTION, AND THERAPY OF BREAST CANCER  
FILE REFERENCE: MRI-038  
CURRENT APPLICATION NUMBER: US/10/177,293  
CURRENT FILING DATE: 2002-06-21  
PRIOR APPLICATION NUMBER: US 60/299,887  
PRIOR FILING DATE: 2001-06-21  
PRIOR APPLICATION NUMBER: US 60/301,572  
PRIOR FILING DATE: 2001-06-27  
PRIOR APPLICATION NUMBER: US 60/306,501  
PRIOR FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: US 60/325,002  
PRIOR FILING DATE: 2001-09-25  
PRIOR APPLICATION NUMBER: US 60/362,585  
PRIOR FILING DATE: 2002-03-05  
PRIOR APPLICATION NUMBER: US 60/xxx,xxx

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/ PRIOR FILING DATE: 2002-05-14
/ NUMBER OF SEQ ID NOS: 506
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 124
/ LENGTH: 434
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-177-293-124

Query Match      72.2%  Score 65;  DB 4;  Length 434;
Best Local Similarity 81.2%  Pred. No. 0.41;
Matches 13;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

Qy      1  LVVGLCTCQIKTGAPC 16
Db      384 LVVGLCTCQIKTGAPC 399

RESULT 15
US-10-205-194-47
/ Sequence 47, Application US/10205194
/ Publication No. US20030134301A1
/ GENERAL INFORMATION:
/ APPLICANT: Warner-Lambert Company
/ APPLICANT: Lee, Kevin
/ APPLICANT: Dixon, Alstair
/ APPLICANT: Brookabank, Robert
/ APPLICANT: Plimock, Robert
/ TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
/ FILE REFERENCE: WI-A-018201
/ CURRENT APPLICATION NUMBER: US/10/205,194
/ PRIOR FILING DATE: 5200-07-24
/ PRIOR APPLICATION NUMBER: GB 0118354.0
/ PRIOR FILING DATE: 2001-07-27
/ NUMBER OF SEQ ID NOS: 177
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 47
/ LENGTH: 434
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
/ FEATURE:
/ OTHER INFORMATION: Neuron-specific enolase
US-10-205-194-47

Query Match      72.2%  Score 65;  DB 4;  Length 434;
Best Local Similarity 81.2%  Pred. No. 0.41;
Matches 13;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

Qy      1  LVVGLCTCQIKTGAPC 16
Db      384 LVVGLCTCQIKTGAPC 399

RESULT 16
US-10-354-358-16
/ Sequence 16, Application US/10354358
/ Publication No. US20030157082A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc
/ APPLICANT: Hunter, John Joseph
/ APPLICANT: MacBeth, Kyle J.
/ APPLICANT: Teal, Fong-ying
/ APPLICANT: Lesoon, Andrea
/ APPLICANT: Lightcap, Eric S.
/ APPLICANT: Williamsen, Mark
/ APPLICANT: Rudolph-Owen, Laura A.
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
/ TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
/ TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
/ TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
/ TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
/ TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
/ TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
```

```
/ TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
/ FILE REFERENCE: MP102-020P/RNOMNIM
/ CURRENT APPLICATION NUMBER: US/10/354,358
/ CURRENT FILING DATE: 2003-01-30
/ PRIOR APPLICATION NUMBER: US 60/353,600
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 60/364,517
/ PRIOR FILING DATE: 2002-03-15
/ PRIOR APPLICATION NUMBER: US 60/371,075
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: US 60/371,507
/ PRIOR FILING DATE: 2002-04-10
/ PRIOR APPLICATION NUMBER: US 60/372,984
/ PRIOR FILING DATE: 2002-04-16
/ PRIOR APPLICATION NUMBER: US 60/374,194
/ PRIOR FILING DATE: 2002-04-19
/ PRIOR APPLICATION NUMBER: US 60/382,995
/ PRIOR FILING DATE: 2002-05-24
/ PRIOR APPLICATION NUMBER: US 60/385,023
/ PRIOR FILING DATE: 2002-05-31
/ PRIOR APPLICATION NUMBER: US 60/388,853
/ PRIOR FILING DATE: 2002-06-14
/ PRIOR APPLICATION NUMBER: US 60/389,395
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 122
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 16
/ LENGTH: 434
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-354-358-16

Query Match      72.2%  Score 65;  DB 4;  Length 434;
Best Local Similarity 81.2%  Pred. No. 0.41;
Matches 13;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

Qy      1  LVVGLCTCQIKTGAPC 16
Db      384 LVVGLCTCQIKTGAPC 399

RESULT 17
US-10-170-385-257
/ Sequence 257, Application US/10170385
/ Publication No. US20030203372A1
/ GENERAL INFORMATION:
/ APPLICANT: Ward, Neil Raymond
/ APPLICANT: Mundy, Christopher Robert
/ APPLICANT: Kan, On
/ APPLICANT: Harris, Robert Alan
/ APPLICANT: White, Jonathan
/ APPLICANT: Binley, Katie Mary
/ APPLICANT: Rayner, William Nigel
/ APPLICANT: Naylor, Stuart
/ APPLICANT: Kingsman, Susan Mary
/ APPLICANT: Krige, David
/ TITLE OF INVENTION: ANALYSIS METHOD
/ FILE REFERENCE: 532682000100
/ CURRENT APPLICATION NUMBER: US/10/170,385
/ CURRENT FILING DATE: 2002-06-12
/ PRIOR APPLICATION NUMBER: PCT/GB02/01662
/ PRIOR FILING DATE: 2002-04-08
/ PRIOR APPLICATION NUMBER: PCT/GB01/05458
/ PRIOR FILING DATE: 2001-12-10
/ NUMBER OF SEQ ID NOS: 549
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 257
/ LENGTH: 434
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-170-385-257
```

Query Match 72.2%; Score 65; DB 4; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.41;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 384 LVVGLCTGQIKTGAPC 399

RESULT 18  
US-10-170-385-273  
Sequence 273, Application US/10170385  
Publication No. US20030203372A1  
GENERAL INFORMATION:  
APPLICANT: Ward, Neil Raymond  
APPLICANT: Mundy, Christopher Robert  
APPLICANT: Kan, On  
APPLICANT: Harris, Robert Alan  
APPLICANT: White, Jonathan  
APPLICANT: Binley, Katie Mary  
APPLICANT: Rayner, William Nigel  
APPLICANT: Naylor, Stuart  
APPLICANT: Kingman, Susan Mary  
APPLICANT: Krige, David  
TITLE OF INVENTION: ANALYSIS METHOD  
FILE REFERENCE: 532682000100  
CURRENT APPLICATION NUMBER: US/10/170,385  
CURRENT FILING DATE: 2002-06-12  
PRIOR APPLICATION NUMBER: PCT/GB02/01662  
PRIOR FILING DATE: 2002-04-08  
PRIOR APPLICATION NUMBER: PCT/GB01/05458  
PRIOR FILING DATE: 2001-12-10  
NUMBER OF SEQ ID NOS: 549  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 273  
LENGTH: 434  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-10-170-385-273

Query Match 72.2%; Score 65; DB 4; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.41;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 384 LVVGLCTGQIKTGAPC 399

RESULT 19  
US-10-258-666-10  
Sequence 10, Application US/10258666  
Publication No. US20040005578A1  
GENERAL INFORMATION:  
APPLICANT: Yamada, Yoji  
APPLICANT: Sekine, Susumu  
APPLICANT: Kikuchi, Yasuhiro  
APPLICANT: Sakurada, Kazuhito  
APPLICANT: Kyowa Hakko Kogyo Co., Ltd.  
TITLE OF INVENTION: Myocardial Cell Proliferation-Associated Genes  
FILE REFERENCE: 082382-000000US  
CURRENT APPLICATION NUMBER: US/10/258,666  
CURRENT FILING DATE: 2003-05-23  
PRIOR APPLICATION NUMBER: JP 2000-126741  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: WO PCT/JP01/03700  
PRIOR FILING DATE: 2001-04-27  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 10  
LENGTH: 434  
TYPE: PRT  
ORGANISM: Rattus norvegicus

FEATURE:  
OTHER INFORMATION: RHDH-099, non-neuronal enolase  
US-10-258-666-10

Query Match 72.2%; Score 65; DB 4; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.41;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 384 LVVGLCTGQIKTGAPC 399

RESULT 20  
US-10-205-331-26  
Sequence 26, Application US/10205331  
Publication No. US20040058326A1  
GENERAL INFORMATION:  
APPLICANT: Warner-Lambert Company  
APPLICANT: Lee, Kevin  
APPLICANT: Dixon, Alistair  
APPLICANT: Brooksbank, Robert  
APPLICANT: Pincock, Robert  
TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain  
FILE REFERENCE: WL-A-018199  
CURRENT APPLICATION NUMBER: US/10/205,331  
CURRENT FILING DATE: 2002-07-24  
PRIOR APPLICATION NUMBER: GB 0118354.0  
PRIOR FILING DATE: 2001-07-27  
NUMBER OF SEQ ID NOS: 117  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 26  
LENGTH: 434  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Alpha-enolase  
US-10-205-331-26

Query Match 72.2%; Score 65; DB 4; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.41;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16  
DB 384 LVVGLCTGQIKTGAPC 399

RESULT 21  
US-10-473-127-595  
Sequence 595, Application US/10473127  
Publication No. US20040236091A1  
GENERAL INFORMATION:  
APPLICANT: Zycoos Inc.  
TITLE OF INVENTION: TRANSLATIONAL PROFILING  
FILE REFERENCE: 08191-026W01  
CURRENT APPLICATION NUMBER: US/10/473,127  
CURRENT FILING DATE: 2003-09-26  
PRIOR APPLICATION NUMBER: 60/279,495  
PRIOR FILING DATE: 2001-03-28  
PRIOR APPLICATION NUMBER: 60/292,544  
PRIOR FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: 60/310,801  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: 60/326,370  
PRIOR FILING DATE: 2001-10-01  
PRIOR APPLICATION NUMBER: 60/336,780  
PRIOR FILING DATE: 2001-12-04  
PRIOR APPLICATION NUMBER: 60/358,985  
PRIOR FILING DATE: 2002-02-20  
NUMBER OF SEQ ID NOS: 2041  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 595

```
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-595
```

```
Query Match          72.2% Score 65; DB 5; Length 434;
Best Local Similarity 81.2% Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 LVVGLCTGQIKTGAPC 16
Db      384 LVVGLCTGQIKTGAPC 399
```

```
RESULT 22
US-10-473-127-596
; Sequence 596, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/232,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 596
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-596
```

```
Query Match          72.2% Score 65; DB 5; Length 434;
Best Local Similarity 81.2% Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 LVVGLCTGQIKTGAPC 16
Db      384 LVVGLCTGQIKTGAPC 399
```

```
RESULT 23
US-10-473-127-597
; Sequence 597, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
```

```
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 597
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-597
```

```
Query Match          72.2% Score 65; DB 5; Length 434;
Best Local Similarity 81.2% Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 LVVGLCTGQIKTGAPC 16
Db      384 LVVGLCTGQIKTGAPC 399
```

```
RESULT 24
US-10-473-127-598
; Sequence 598, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 598
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-598
```

```
Query Match          72.2% Score 65; DB 5; Length 434;
Best Local Similarity 81.2% Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 LVVGLCTGQIKTGAPC 16
Db      384 LVVGLCTGQIKTGAPC 399
```

```
RESULT 25
US-10-473-127-599
; Sequence 599, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
```



```
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 599
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-599
```

```
Query Match      72.2%; Score 65; DB 5; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Oy 1 LVVGLCTGQIKTGAPC 16
Db 384 LVVGLCTGQIKTGAPC 399
```

```
RESULT 26
US-10-473-127-600
; Sequence 600, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 600
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-600
```

```
Query Match      72.2%; Score 65; DB 5; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Oy 1 LVVGLCTGQIKTGAPC 16
Db 384 LVVGLCTGQIKTGAPC 399
```

```
RESULT 27
US-10-473-127-601
; Sequence 601, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
```

```
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 601
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-601
```

```
Query Match      72.2%; Score 65; DB 5; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Oy 1 LVVGLCTGQIKTGAPC 16
Db 384 LVVGLCTGQIKTGAPC 399
```

```
RESULT 28
US-10-473-127-602
; Sequence 602, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 602
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-602
```

```
Query Match      72.2%; Score 65; DB 5; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Oy 1 LVVGLCTGQIKTGAPC 16
Db 384 LVVGLCTGQIKTGAPC 399
```

```
RESULT 29
US-10-473-127-603
; Sequence 603, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
```

Search completed: April 3, 2006, 08:17:02  
Job time : 168 secs

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; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 603
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-603

```

```

Query Match          72.2%; Score 65; DB 5; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      1 LVVGLCTGQIKTGAPC 16
DB      384 LVVGLCTGQIKTGAPC 399

```

```

RESULT 30
US-10-473-127-609
; Sequence 609, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 609
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-609

```

```

Query Match          72.2%; Score 65; DB 5; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.41;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      1 LVVGLCTGQIKTGAPC 16
DB      384 LVVGLCTGQIKTGAPC 399

```

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: Apr11 3, 2006, 08:07:10 ; Search time 12 Seconds  
(without alignments)  
40.589 Million cell updates/sec

Title: US-09-647-457F-3  
Perfect score: 90  
Sequence: 1 LVWGLCTCQIKTGPAAC 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues  
Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications AA-New:\*  
1: /SIDS/prodata/1/pubppa/US08\_NEW\_PUB pep:\*  
2: /SIDS/prodata/1/pubppa/US06\_NEW\_PUB pep:\*  
3: /SIDS/prodata/1/pubppa/US07\_NEW\_PUB pep:\*  
4: /SIDS/prodata/1/pubppa/PCT\_NEW\_PUB pep:\*  
5: /SIDS/prodata/1/pubppa/US09\_NEW\_PUB pep:\*  
6: /SIDS/prodata/1/pubppa/US10\_NEW\_PUB pep:\*  
7: /SIDS/prodata/1/pubppa/US11\_NEW\_PUB pep:\*  
8: /SIDS/prodata/1/pubppa/US60\_NEW\_PUB pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	82.2	458	6	US-10-878-556A-28 Sequence 28, Appl
2	65	72.2	434	6	US-10-821-234-1553 Sequence 1553, Ap
3	65	72.2	434	7	US-11-168-637-10 Sequence 10, Appl
4	47.5	52.8	1620	6	US-10-055-877-213 Sequence 213, Appl
5	47.5	52.8	1664	6	US-10-055-877-212 Sequence 212, Appl
6	46	51.1	46	7	US-11-068-783-111 Sequence 111, Appl
7	45.5	50.6	127	7	US-11-172-740-2156 Sequence 2156, Appl
8	43	47.8	100	7	US-11-043-693-51 Sequence 51, Appl
9	43	47.8	452	7	US-11-016-503-6 Sequence 6, Appl
10	43	47.8	462	7	US-11-016-503-8 Sequence 8, Appl
11	43	47.8	557	7	US-11-016-503-4 Sequence 4, Appl
12	43	47.8	567	7	US-11-016-503-2 Sequence 2, Appl
13	43	47.8	567	7	US-11-016-503-10 Sequence 10, Appl
14	43	47.8	758	7	US-11-043-693-11 Sequence 11, Appl
15	43	47.8	1338	6	US-10-821-234-1522 Sequence 1622, Appl
16	43	47.8	1338	7	US-11-109-136-23 Sequence 23, Appl
17	43	47.8	1338	7	US-11-075-047A-2 Sequence 2, Appl
18	43	47.8	1362	7	US-11-043-693-33 Sequence 33, Appl
19	42	46.7	296	7	US-11-182-343-31 Sequence 31, Appl
20	42	46.7	360	7	US-11-112-240-1 Sequence 1, Appl
21	42	46.7	360	7	US-11-112-304A-1 Sequence 1, Appl
22	42	46.7	544	6	US-10-980-388-40 Sequence 40, Appl
23	41	45.6	839	7	US-11-096-568A-24462 Sequence 24462, A
24	41	45.6	878	7	US-11-096-568A-24461 Sequence 24461, A
25	41	45.6	909	7	US-11-096-568A-24460 Sequence 24460, A

26	40.5	45.0	1433	7	US-11-114-962-1 Sequence 1, Appl
27	40.5	45.0	2556	7	US-11-050-346-67 Sequence 67, Appl
28	40	44.4	205	6	US-10-793-626-2510 Sequence 2510, Ap
29	40	44.4	1356	6	US-10-894-592-3 Sequence 3, Appl
30	39.5	43.9	257	7	US-11-096-051-12 Sequence 12, Appl
31	39.5	43.9	296	7	US-11-096-051-18 Sequence 18, Appl
32	39.5	43.9	821	7	US-11-096-051-6 Sequence 6, Appl
33	39.5	43.9	862	7	US-11-096-051-20 Sequence 20, Appl
34	39.5	43.9	2376	7	US-11-096-051-4 Sequence 4, Appl
35	39.5	43.9	2715	7	US-11-096-051-2 Sequence 2, Appl
36	39.5	43.9	2725	7	US-11-096-051-10 Sequence 10, Appl
37	39.5	43.9	2725	7	US-11-096-051-8 Sequence 8, Appl
38	39	43.3	905	7	US-11-072-512-2728 Sequence 2728, Ap
39	38.5	42.8	1400	6	US-10-821-234-1045 Sequence 1045, Ap
40	38.5	42.8	1574	6	US-10-055-877-211 Sequence 211, Appl
41	38.5	42.8	2715	7	US-11-113-424-51 Sequence 51, Appl
42	38.5	42.8	3597	7	US-11-019-711-6 Sequence 6, Appl
43	38.5	42.8	3600	7	US-11-019-711-2 Sequence 2, Appl
44	38.5	42.8	3690	6	US-10-995-561-1015 Sequence 1015, Ap
45	38.5	42.8	3714	6	US-10-995-561-1016 Sequence 1016, Ap
46	38.5	42.8	3717	6	US-10-821-234-1076 Sequence 1076, Ap
47	38	42.2	27	6	US-10-895-861-30 Sequence 30, Appl
48	38	42.2	162	7	US-11-096-568A-9458 Sequence 9458, Ap
49	38	42.2	186	7	US-11-096-568A-9457 Sequence 9457, Ap
50	38	42.2	461	7	US-11-132-285-6 Sequence 6, Appl
51	38	42.2	461	7	US-11-182-946-4 Sequence 4, Appl
52	38	42.2	461	7	US-11-182-205-32 Sequence 32, Appl
53	38	42.2	627	6	US-10-330-773-78 Sequence 78, Appl
54	38	42.2	1683	7	US-11-131-479-38 Sequence 38, Appl
55	37.5	41.7	176	7	US-11-128-059-72 Sequence 72, Appl
56	37.5	41.7	232	7	US-11-128-059-66 Sequence 66, Appl
57	37.5	41.7	244	6	US-10-453-372-214 Sequence 214, Appl
58	37.5	41.7	315	6	US-10-453-372-212 Sequence 212, Appl
59	37.5	41.7	421	6	US-10-453-372-220 Sequence 220, Appl
60	37.5	41.7	533	6	US-10-453-372-230 Sequence 230, Appl
61	37.5	41.7	533	6	US-10-453-372-232 Sequence 232, Appl
62	37.5	41.7	539	7	US-11-183-136-38 Sequence 38, Appl
63	37.5	41.7	552	6	US-10-453-372-234 Sequence 234, Appl
64	37.5	41.7	552	6	US-10-453-372-236 Sequence 236, Appl
65	37.5	41.7	552	6	US-10-453-372-238 Sequence 238, Appl
66	37.5	41.7	552	6	US-10-453-372-240 Sequence 240, Appl
67	37.5	41.7	552	6	US-10-453-372-242 Sequence 242, Appl
68	37.5	41.7	552	6	US-10-453-372-244 Sequence 244, Appl
69	37.5	41.7	552	6	US-10-453-372-246 Sequence 246, Appl
70	37.5	41.7	552	6	US-10-453-372-248 Sequence 248, Appl
71	37.5	41.7	552	6	US-10-453-372-250 Sequence 250, Appl
72	37.5	41.7	552	6	US-10-453-372-252 Sequence 252, Appl
73	37.5	41.7	552	6	US-10-453-372-254 Sequence 254, Appl
74	37.5	41.7	552	6	US-10-453-372-256 Sequence 256, Appl
75	37.5	41.7	552	6	US-10-453-372-258 Sequence 258, Appl
76	37.5	41.7	552	6	US-10-453-372-260 Sequence 260, Appl
77	37.5	41.7	897	6	US-10-453-372-208 Sequence 88, Appl
78	37.5	41.7	931	7	US-11-128-059-86 Sequence 86, Appl
79	37.5	41.7	1198	6	US-10-453-372-880 Sequence 880, Appl
80	37.5	41.7	1327	7	US-11-128-059-92 Sequence 92, Appl
81	37.5	41.7	1327	7	US-11-128-059-94 Sequence 94, Appl
82	37.5	41.7	1398	6	US-10-055-877-46 Sequence 46, Appl
83	37.5	41.7	1398	6	US-10-453-372-872 Sequence 872, Appl
84	37.5	41.7	1403	6	US-10-055-877-52 Sequence 52, Appl
85	37.5	41.7	1403	6	US-10-453-372-878 Sequence 878, Appl
86	37.5	41.7	1404	6	US-10-055-877-44 Sequence 44, Appl
87	37.5	41.7	1404	6	US-10-453-372-870 Sequence 870, Appl
88	37.5	41.7	1416	6	US-11-128-059-4 Sequence 4, Appl
89	37.5	41.7	1418	6	US-10-453-372-864 Sequence 864, Appl
90	37.5	41.7	1450	6	US-10-055-877-48 Sequence 48, Appl
91	37.5	41.7	1450	6	US-10-453-372-874 Sequence 874, Appl
92	37.5	41.7	1502	6	US-10-453-372-252 Sequence 252, Appl
93	37.5	41.7	1510	6	US-10-453-372-254 Sequence 254, Appl
94	37.5	41.7	1547	6	US-10-453-372-886 Sequence 886, Appl
95	37.5	41.7	1577	6	US-10-055-877-54 Sequence 54, Appl
96	37.5	41.7	1577	6	US-10-453-372-882 Sequence 882, Appl
97	37.5	41.7	1577	6	US-10-453-372-884 Sequence 884, Appl
98	37.5	41.7	1594	6	US-10-453-372-860 Sequence 860, Appl

99 37.5 41.7 1609 7 US-11-072-175-185  
100 37.5 41.7 1616 6 US-10-821-234-1497

Sequence 185, App  
Sequence 1497, Ap

## ALIGNMENTS

RESULT 1  
US-10-878-556A-28

Sequence 28, Application US/10878556A  
Publication No. US2005026399A1  
GENERAL INFORMATION:  
APPLICANT: Hoffmann La-Roche Inc.  
TITLE OF INVENTION: HCV regulated protein expression  
FILE REFERENCE: 21762  
CURRENT APPLICATION NUMBER: US/10/878,556A  
CURRENT FILING DATE: 2004-06-28  
NUMBER OF SEQ ID NOS: 199  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 28  
LENGTH: 458  
TYPE: PRT  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: sw\_hum/enol\_human  
DATABASE ENTRY DATE: 1995-02-01  
US-10-878-556A-28

## Query Match

Best Local Similarity 82.2%; Score 74; DB 6; Length 458;  
Best Local Similarity 87.5%; Pred. No. 0.00019;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16

Db 407 LVVGLCTGQIKTGPTC 422

## RESULT 2

US-10-821-234-1553  
Sequence 1553, Application US/10821234  
Publication No. US2005025511A1  
GENERAL INFORMATION:  
APPLICANT: Labat, Ivan  
APPLICANT: Stache-Crain, Brigitte  
APPLICANT: Andaman, Susan  
APPLICANT: Tang, Y. Tom  
FILE REFERENCE: 821A  
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
CURRENT APPLICATION NUMBER: US/10/821,234  
CURRENT FILING DATE: 2004-04-07  
PRIOR APPLICATION NUMBER: US 60/462,047  
PRIOR FILING DATE: 2003-04-07  
NUMBER OF SEQ ID NOS: 1704  
SOFTWARE: pc\_seq\_genes Version 1.0  
SEQ ID NO: 1553  
LENGTH: 434  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-821-234-1553

## Query Match

Best Local Similarity 72.2%; Score 65; DB 6; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.0049;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16

Db 384 LVVGLCTGQIKTGAPC 399

## RESULT 3

US-11-168-637-10  
Sequence 10, Application US/11168637  
Publication No. US2006005174A1

GENERAL INFORMATION:  
APPLICANT: Austen, Kimberly M.  
APPLICANT: Kapil, Sanjay  
APPLICANT: Kim, Jeong-Ki

TITLE OF INVENTION: FELINE INFECTIOUS PERITONITIS (FIP) AND  
SYSTEMIC MULTI-ORGAN CORONAVIRUS BIOMARKERS AND SCREENING  
METHODS  
FILE REFERENCE: 14337-005001  
CURRENT APPLICATION NUMBER: US/11/168,637  
CURRENT FILING DATE: 2005-06-28  
PRIOR APPLICATION NUMBER: US 60/656,027  
PRIOR FILING DATE: 2005-02-24  
PRIOR APPLICATION NUMBER: US 60/584,439  
PRIOR FILING DATE: 2004-06-20  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 10  
LENGTH: 434  
TYPE: PRT  
ORGANISM: Felis catus  
US-11-168-637-10

## Query Match

Best Local Similarity 72.2%; Score 65; DB 7; Length 434;  
Best Local Similarity 81.2%; Pred. No. 0.0049;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16

Db 384 LVVGLCTGQIKTGAPC 399

## RESULT 4

US-10-055-877-213  
Sequence 213, Application US/10055877  
Publication No. US20050288241A1  
GENERAL INFORMATION:  
APPLICANT: Decristofaro, Marc  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Miller, Charles  
APPLICANT: Tchernev, Velizar  
APPLICANT: Zhong, Mei  
APPLICANT: Anderson, David  
APPLICANT: Ballinger, Robert  
APPLICANT: Gerlach, Valerie  
APPLICANT: Spyrek, Kimberly  
APPLICANT: Patel, Luca  
APPLICANT: Kekuda, Rameen  
APPLICANT: Guo, Xiaojia  
APPLICANT: Zernusen, Bryan  
APPLICANT: Andrew, David  
APPLICANT: Mezes, Peter  
APPLICANT: Patturajan, Meera  
APPLICANT: Burgess, Catherine  
APPLICANT: Eiben, Andrew  
APPLICANT: Wolenc, Adam  
APPLICANT: Baumgartner, Jason  
APPLICANT: Shinkets, Richard  
APPLICANT: Gusev, Vladimir  
APPLICANT: Vernet, Corine  
APPLICANT: Taupier, Jr., Raymond  
APPLICANT: Pena, Carol  
APPLICANT: Shenoy, Suresh  
APPLICANT: Li, Li  
APPLICANT: Casman, Stracie  
APPLICANT: Boldog, Renée  
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby  
FILE REFERENCE: 21402-251  
CURRENT APPLICATION NUMBER: US/10/055,877  
CURRENT FILING DATE: 2002-01-22  
PRIOR APPLICATION NUMBER: 60/262,892  
PRIOR FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: 60/263,598  
PRIOR FILING DATE: 2001-01-23

```

; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 213
; LENGTH: 1620
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-10-055-877-213

Query Match      52.8%; Score 47.5; DB 6; Length 1620;
Best Local Similarity 62.5%; Pred. No. 9.2;
Matches 10; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy      2  VVGLCTC-QIKTGPAC 16
Db      876 VTGCTCTCLPGKTGPLC 891

RESULT 5
; Sequence 212, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratek, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zernusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patcurajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkete, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corinne
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892

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; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 212
; LENGTH: 1664
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-10-055-877-212

Query Match      52.8%; Score 47.5; DB 6; Length 1664;
Best Local Similarity 62.5%; Pred. No. 9.4;
Matches 10; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy      2  VVGLCTC-QIKTGPAC 16
Db      828 VTGCTCTCLPGKTGPLC 843

RESULT 6
; Sequence 111, Application US/11068783
; Publication No. US20050260715A1
; GENERAL INFORMATION:
; APPLICANT: Burian, Jan
; APPLICANT: Bartfeld, Daniel
; TITLE OF INVENTION: EFFICIENT METHODS FOR PRODUCING
; FILE REFERENCE: 660081.411
; CURRENT APPLICATION NUMBER: US/11/068,783
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US/09/444,281
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Hordeum vulgare
; US-11-068-783-111

Query Match      51.1%; Score 46; DB 7; Length 46;
Best Local Similarity 53.8%; Pred. No. 0.67;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      4  GLCTCQIKTGPAC 16
Db      28 GACRCKITSGPKC 40

RESULT 7
; Sequence 2156, Application US/11172740
; Publication No. US20060057724A1
; GENERAL INFORMATION:

```

```
/ APPLICANT: MASCIA, Peter
/ APPLICANT: ALEXANDROV, Nikolai
/ APPLICANT: BROVER, Vvacheklav
/ TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR
/ TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
/ FILE REFERENCE: 2750-1602PUS2
/ CURRENT APPLICATION NUMBER: US/11/172,740
/ CURRENT FILING DATE: 2005-06-30
/ PRIOR APPLICATION NUMBER: 60/583,621
/ PRIOR FILING DATE: 2004-06-30
/ PRIOR APPLICATION NUMBER: 60/584,829
/ PRIOR FILING DATE: 2004-06-30
/ PRIOR APPLICATION NUMBER: 60/584,800
/ PRIOR FILING DATE: 2004-06-30
/ NUMBER OF SEQ ID NOS: 2523
/ SEQ ID NO 2156
/ LENGTH: 127
/ TYPE: PRT
/ ORGANISM: Arabidopsis thaliana
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)-(127)
/ OTHER INFORMATION: Public GI no. 46396244
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: Utility: Useful for making plants sterile and for genetic confine
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: Utility: Useful for making smaller plants
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: Utility: Useful for making stronger plants
/ US-11-172-740-2156

Query Match      50.6%; Score 45.5; DB 7; Length 127;
Best Local Similarity 47.4%; Pred. No. 2;
Matches 9; Conservative 2; Mismatches 3; Indels 5; Gaps 1;

QY      3  VGLC-----TCQIKTGPAC 16
      :|||:|||||:
Db      33  LGLCETCDERCQAHGFGSC 51

RESULT 8
US-11-043-693-51
/ Sequence 51, Application US/11043693
/ Publication No. US20050281831A1
/ GENERAL INFORMATION:
/ APPLICANT: Davis-Smyth, Terri L.
/ APPLICANT: Chen, Helen H.
/ APPLICANT: Presta, Leonardo
/ APPLICANT: Ferrara, Napoleone
/ TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL
/ TITLE OF INVENTION: GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR
/ TITLE OF INVENTION: PRODUCTION
/ NUMBER OF SEQUENCES: 52
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Dorsey & Whitney LLP
/ STREET: Four Embarcadero Center, Suite 3400
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States
/ ZIP: 94111-4187
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/11/043,693
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/ FILING DATE: 26-Jan-2005
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/10/105,901
/ FILING DATE: 20-Mar-2002
/ APPLICATION NUMBER: 09/348,886
/ FILING DATE: 01-JUL-1999
/ APPLICATION NUMBER: US 08/643,839
/ FILING DATE: 07-MAY-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Richard F. Trecartin
/ REGISTRATION NUMBER: 31,801
/ REFERENCE/DOCKET NUMBER: A-63291-3/RFT/NBC
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 781-1989
/ TELEFAX: (415) 398-3249
/ TELEX: 910 277299
/ INFORMATION FOR SEQ ID NO: 51:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 100 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-11-043-693-51

Query Match      47.8%; Score 43; DB 7; Length 100;
Best Local Similarity 50.0%; Pred. No. 4;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      4  GLCTCQIKTGP 15
      :|||:|||||:
Db      192  GLYTCRVRSGPS 203

RESULT 10
US-11-016-503-8
/ Sequence 8, Application US/11016503
```

```
/ Publication No. US20050245447A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
; FILE REFERENCE: REG 710-A-US
; CURRENT APPLICATION NUMBER: US/11/016,503
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: US/10/009,852
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-016-503-8

Query Match          47.8%; Score 43; DB 7; Length 462;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 15
DB 202 GLYTCRVSGPS 213

RESULT 11
US-11-016-503-4
; Sequence 4, Application US/11016503
; Publication No. US20050245447A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
; FILE REFERENCE: REG 710-A-US
; CURRENT APPLICATION NUMBER: US/11/016,503
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: US/10/009,852
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-016-503-4

Query Match          47.8%; Score 43; DB 7; Length 557;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 15
DB 297 GLYTCRVSGPS 308

RESULT 12
US-11-016-503-2
; Sequence 2, Application US/11016503
; Publication No. US20050245447A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
```

```
/ TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
; FILE REFERENCE: REG 710-A-US
; CURRENT APPLICATION NUMBER: US/11/016,503
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: US/10/009,852
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-016-503-2

Query Match          47.8%; Score 43; DB 7; Length 567;
Best Local Similarity 50.0%; Pred. No. 19;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 15
DB 307 GLYTCRVSGPS 318

RESULT 13
US-11-016-503-10
; Sequence 10, Application US/11016503
; Publication No. US20050245447A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
; FILE REFERENCE: REG 710-A-US
; CURRENT APPLICATION NUMBER: US/11/016,503
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: US/10/009,852
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-016-503-10

Query Match          47.8%; Score 43; DB 7; Length 567;
Best Local Similarity 50.0%; Pred. No. 19;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 15
DB 307 GLYTCRVSGPS 318

RESULT 14
US-11-043-693-1
; Sequence 1, Application US/11043693
; Publication No. US20050281831A1
; GENERAL INFORMATION:
; APPLICANT: Davis-Smyth, Terri L.
; APPLICANT: Chen, Helen H.
; APPLICANT: Presta, Leonard
; APPLICANT: Ferrara, Napoleone
```

```
/ TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL
/ TITLE OF INVENTION: GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR
/ TITLE OF INVENTION: PRODUCTION
/ NUMBER OF SEQUENCES: 52
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Doreay & Whitney LLP
/ STREET: Four Embarcadero Center, Suite 3400
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States
/ ZIP: 94111-4187
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/11/043,693
/ FILING DATE: 26-Jan-2005
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/10/105,901
/ FILING DATE: 20-Mar-2002
/ APPLICATION NUMBER: 09/348,886
/ FILING DATE: 01-JUL-1999
/ APPLICATION NUMBER: US 08/643,839
/ FILING DATE: 07-MAY-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Richard F. Trecartin
/ REGISTRATION NUMBER: 31,801
/ REFERENCE/DOCKET NUMBER: A-63291-3/RPT/NEC
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 781-1989
/ TELEFAX: (415) 398-3249
/ TELETEXT: 910 277299
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 758 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-11-043-693-1

Query Match      47.8%; Score 43; DB 7; Length 758;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
/ ORGANISM: Homo sapiens
/ US-10-821-234-1622

Query Match      47.8%; Score 43; DB 6; Length 1338;
Best Local Similarity 50.0%; Pred. No. 40;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 GLCTCQIKTGPA 15
Db      307 GLYTCRVRSGPS 318

RESULT 16
US-11-109-156-23
/ Sequence 23, Application US/1109156
/ Publication No. US20050250144A1
/ GENERAL INFORMATION:
/ APPLICANT: Toshio Ota
/ APPLICANT: Takao Isogai
/ APPLICANT: Tetsuo Nishikawa
/ APPLICANT: Koji Hayashi
/ APPLICANT: Kaoru Otsuka
/ APPLICANT: Jun-ichi Yamamoto
/ APPLICANT: Shizuko Ishii
/ APPLICANT: Tomoyasu Sugiyama
/ APPLICANT: Ai Wakamatsu
/ APPLICANT: Keiichi Nagai
/ APPLICANT: Tetsuji Otsubki
/ APPLICANT: Shin-ichi Funahashi
/ APPLICANT: Chiaki Senoo
/ APPLICANT: Jun-ichi Nezu
/ TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
/ TITLE OF INVENTION: PHOSPHATASE
/ FILE REFERENCE: 06501-099002
/ CURRENT APPLICATION NUMBER: US/11/109,156
/ PRIOR FILING DATE: 2005-04-19
/ PRIOR APPLICATION NUMBER: US/10/060,065
/ PRIOR FILING DATE: 2002-01-29
/ PRIOR APPLICATION NUMBER: PCT/JP00/05061
/ PRIOR FILING DATE: 2000-07-28
/ PRIOR APPLICATION NUMBER: US 60/159,590
/ PRIOR FILING DATE: 1999-10-18
/ PRIOR APPLICATION NUMBER: US 60/183,322
/ PRIOR FILING DATE: 2000-02-17
/ PRIOR APPLICATION NUMBER: JP 11-248036
/ PRIOR FILING DATE: 1999-07-29
/ PRIOR APPLICATION NUMBER: JP 2000-118776
/ PRIOR FILING DATE: 2000-01-11
/ PRIOR APPLICATION NUMBER: JP 2000-183767
/ PRIOR FILING DATE: 2000-05-02
/ PRIOR APPLICATION NUMBER: JP 2000-241899
/ PRIOR FILING DATE: 2000-06-09
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 23
/ LENGTH: 1338
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-11-109-156-23

Query Match      47.8%; Score 43; DB 7; Length 1338;
Best Local Similarity 50.0%; Pred. No. 40;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 GLCTCQIKTGPA 15
Db      307 GLYTCRVRSGPS 318

RESULT 17
US-11-075-047A-2
/ Sequence 2, Application US/11075047A
/ Publication No. US2006030000A1
```



GENERAL INFORMATION:  
APPLICANT: ALTITALO, et al.  
TITLE OF INVENTION: GROWTH FACTOR BINDING CONSTRUCTS MATERIALS AND METHODS  
FILE REFERENCE: 28967/39700A  
CURRENT APPLICATION NUMBER: US/11/075,047A  
CURRENT FILING DATE: 2005-03-07  
PRIOR APPLICATION NUMBER: US 60/550,907  
PRIOR FILING DATE: 2004-03-07  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 2  
LENGTH: 1338  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-075-047A-2

Query Match 47.8%; Score 43; DB 7; Length 1338;  
Best Local Similarity 50.0%; Pred. No. 40;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLTCQIKTGPA 15  
DB 307 GLYTCRVRSGPS 318

RESULT 18  
US-11-043-693-33  
Sequence 33, Application US/11043693  
Publication No. US20050281831A1  
GENERAL INFORMATION:  
APPLICANT: Davis-Smyth, Terri L.  
APPLICANT: Chen, Helen H.  
APPLICANT: Presta, Leonard  
APPLICANT: Ferrara, Napoleone  
TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL  
TITLE OF INVENTION: GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESSES:  
ADDRESSES: Dorsey & Whitney LLP  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/11/043,693  
FILING DATE: 26-Jan-2005  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/10/105,901  
FILING DATE: 20-Mar-2002  
APPLICATION NUMBER: 09/348,886  
FILING DATE: 01-JUL-1999  
APPLICATION NUMBER: US 08/643,839  
FILING DATE: 07-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Richard F. Treacartn  
REGISTRATION NUMBER: 31,801  
REFERENCE/DOCKET NUMBER: A-63291-3/RFT/NBC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1362 amino acids  
TYPE: amino acid

STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-11-043-693-33

Query Match 47.8%; Score 43; DB 7; Length 1362;  
Best Local Similarity 50.0%; Pred. No. 41;  
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLTCQIKTGPA 15  
DB 305 GLYTCRVRSGPS 316

RESULT 19  
US-11-182-343-31  
Sequence 31, Application US/11182343  
Publication No. US20060018910A1  
GENERAL INFORMATION:  
APPLICANT: Cohen, Bruce  
APPLICANT: Galberro, Antonio  
APPLICANT: Melvin, Carlie  
APPLICANT: Roberts, Luisa M.  
TITLE OF INVENTION: COMBINATION TREATMENT FOR BREAST CANCER  
FILE REFERENCE: PC32226A  
CURRENT APPLICATION NUMBER: US/11/182,343  
CURRENT FILING DATE: 2005-07-15  
PRIOR APPLICATION NUMBER: 60/588,721  
PRIOR FILING DATE: 2004-07-16  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: Patentin version 3.3  
SEQ ID NO 31  
LENGTH: 296  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-182-343-31

Query Match 46.7%; Score 42; DB 7; Length 296;  
Best Local Similarity 53.8%; Pred. No. 15;  
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 GLTCQIKTGPA 16  
DB 56 GACTCTCCTGTGC 68

RESULT 20  
US-11-112-240-1  
Sequence 1, Application US/11112240  
Publication No. US20050287140A1  
GENERAL INFORMATION:  
APPLICANT: Smothers, James F.  
APPLICANT: Fanelow III, William C.  
APPLICANT: Kariv, Revital  
TITLE OF INVENTION: ANTIBODIES OF ANGIOGENESIS INHIBITING DOMAINS OF CD148  
FILE REFERENCE: A-953A(US)  
CURRENT APPLICATION NUMBER: US/11/112,240  
CURRENT FILING DATE: 2005-04-21  
PRIOR APPLICATION NUMBER: 60/564,885  
PRIOR FILING DATE: 2004-04-23  
PRIOR APPLICATION NUMBER: US 60/585,885  
PRIOR FILING DATE: 2004-07-06  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 1  
LENGTH: 360  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-112-240-1

Query Match 46.7%; Score 42; DB 7; Length 360;  
Best Local Similarity 53.8%; Pred. No. 18;  
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGAPAC 16  
| | | | |  
Db 56 GACTCTCTCTGTGC 68

RESULT 21  
US-11-112-304A-1  
; Sequence 1, Application US/11112304A  
; Publication No. US20060002931A1  
; GENERAL INFORMATION:  
; APPLICANT: AMGEN, INC.  
; APPLICANT: Amgen, Inc.  
; APPLICANT: Smothers, James  
; APPLICANT: Farnlow III, William C.  
; APPLICANT: Kariiv, Revital  
; TITLE OF INVENTION: ANTIBODIES OF ANGIOGENESIS INHIBITING DOMAINS OF CD148  
; FILE REFERENCE: 3447  
; CURRENT APPLICATION NUMBER: US/11/112.304A  
; CURRENT FILING DATE: 2005-04-22  
; PRIOR APPLICATION NUMBER: US 60/565,158  
; PRIOR FILING DATE: 2004-04-23  
; PRIOR APPLICATION NUMBER: US 60/564,885  
; PRIOR FILING DATE: 2004-04-23  
; PRIOR APPLICATION NUMBER: US 60/571,566  
; PRIOR FILING DATE: 2004-05-14  
; PRIOR APPLICATION NUMBER: US 60/585,686  
; PRIOR FILING DATE: 2004-07-06  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-112-304A-1

Query Match 46.7%; Score 42; DB 7; Length 360;  
Best Local Similarity 53.8%; Pred. No. 18;  
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGAPAC 16  
| | | | |  
Db 56 GACTCTCTCTGTGC 68

RESULT 22  
US-10-980-388-40  
; Sequence 40, Application US/10980388  
; Publication No. US20050255490A1  
; GENERAL INFORMATION:  
; APPLICANT: Vogel, Gabriel  
; APPLICANT: Parodi, Luis A.  
; APPLICANT: Hiebsch, Ronald R.  
; APPLICANT: Lind, Peter  
; APPLICANT: Kaytes, Paul S.  
; APPLICANT: Ruff, Valerie  
; APPLICANT: Huff, Rita M.  
; APPLICANT: Wood, Linda S.  
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl  
; FILE REFERENCE: 00325.US1  
; CURRENT APPLICATION NUMBER: US/10/980,388  
; CURRENT FILING DATE: 2004-11-02  
; PRIOR APPLICATION NUMBER: US/09/791,932  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 60/184,305  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,304  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,303  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,397  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,247

; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/188,880  
; PRIOR FILING DATE: 2000-03-13  
; PRIOR APPLICATION NUMBER: 60/217,369  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/217,370  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/218,492  
; PRIOR FILING DATE: 2000-07-20  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 184  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 40  
; LENGTH: 544  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-980-388-40

Query Match 46.7%; Score 42; DB 6; Length 544;  
Best Local Similarity 53.8%; Pred. No. 26;  
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGAPAC 16  
| | | | |  
Db 276 GCCTCTCAGCTAC 288

RESULT 23  
US-11-096-568A-24462  
; Sequence 24462, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 24462  
; LENGTH: 839  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(839)  
; OTHER INFORMATION: Ceres Seq. ID no. 12435290  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (325)..(325)  
; OTHER INFORMATION: Xaa is any aa, unknown or other  
US-11-096-568A-24462

Query Match 45.6%; Score 41; DB 7; Length 839;  
Best Local Similarity 50.0%; Pred. No. 55;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVGLCTQIKT 12  
| : | | | : | |  
Db 437 LLAGLCTCAVAT 448

RESULT 24  
US-11-096-568A-24461  
; Sequence 24461, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471  
SEQ ID NO 24461  
LENGTH: 878  
TYPE: PRT  
ORGANISM: Zea mays subsp. mays  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)-(878)  
OTHER INFORMATION: Ceres Seq. ID no. 12435289  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (364)-(364)  
OTHER INFORMATION: Xaa is any aa, unknown or other  
US-11-096-568A-24461

Query Match  
Best Local Similarity 45.6%; Score 41; DB 7; Length 878;  
Best Local Similarity 50.0%; Pred. No. 57;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 1 LVGLCTCOIKT 12  
Db 476 LLAGLCTCAVRT 487

RESULT 25  
US-11-096-568A-24460  
Sequence 24460, Application US/11096568A  
Publication No. US20060048240A1  
GENERAL INFORMATION:  
APPLICANT: Alexandrov, Nikolai et al.  
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
FILE REFERENCE: 2750-1592US2  
CURRENT APPLICATION NUMBER: US/11/096,568A  
CURRENT FILING DATE: 2005-04-01  
NUMBER OF SEQ ID NOS: 34471  
SEQ ID NO 24460  
LENGTH: 909  
TYPE: PRT  
ORGANISM: Zea mays subsp. mays  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)-(909)  
OTHER INFORMATION: Ceres Seq. ID no. 12435288  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (395)-(395)  
OTHER INFORMATION: Xaa is any aa, unknown or other  
US-11-096-568A-24460

Query Match  
Best Local Similarity 45.6%; Score 41; DB 7; Length 909;  
Best Local Similarity 50.0%; Pred. No. 59;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 1 LVGLCTCOIKT 12  
Db 507 LLAGLCTCAVRT 518

RESULT 26  
US-11-114-962-1  
Sequence 1, Application US/11114962  
Publication No. US20060030694A1  
GENERAL INFORMATION:  
APPLICANT: Kitajewski, Jan  
APPLICANT: Shawber, Carrie  
TITLE OF INVENTION: Notch-Based Fusion Proteins And Uses Thereof  
FILE REFERENCE: 0575/71308-A  
CURRENT APPLICATION NUMBER: US/11/114,962  
CURRENT FILING DATE: 2005-04-26  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn version 3.3

SEQ ID NO 1  
LENGTH: 1433  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-11-114-962-1

Query Match  
Best Local Similarity 45.0%; Score 40.5; DB 7; Length 1433;  
Best Local Similarity 61.5%; Pred. No. 11e+02;  
Matches 8; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Oy 5 ICTC-QIKTGPAC 16  
Db 397 ICTCPRGYTGAPAC 409

RESULT 27  
US-11-050-346-67  
Sequence 67, Application US/11050346  
Publication No. US2006002924A1  
GENERAL INFORMATION:  
APPLICANT: BODMER, MARK WILLIAM  
APPLICANT: CHAMPION, BRIAN ROBERT  
APPLICANT: LENNARD, ANDREW CHRISTOPHER  
APPLICANT: MCKENZIE, GRAHAME JAMES  
APPLICANT: TUGAL, TAMARA  
APPLICANT: WARD, GEORGE ALBERT  
TITLE OF INVENTION: NOTCH SIGNALING PATHWAY MODULATORS AND  
FILE REFERENCE: 674525-2016  
CURRENT APPLICATION NUMBER: US/11/050,346  
CURRENT FILING DATE: 2005-02-03  
PRIOR APPLICATION NUMBER: GB 0312062.3  
PRIOR FILING DATE: 2003-05-24  
PRIOR APPLICATION NUMBER: PCT/GB03/01525  
PRIOR FILING DATE: 2003-04-04  
PRIOR APPLICATION NUMBER: GB 0300234.2  
PRIOR FILING DATE: 2003-01-07  
PRIOR APPLICATION NUMBER: GB 0218068.5  
PRIOR FILING DATE: 2002-08-03  
PRIOR APPLICATION NUMBER: GB 0220849.4  
PRIOR FILING DATE: 2002-09-07  
PRIOR APPLICATION NUMBER: GB 0220912.0  
PRIOR FILING DATE: 2002-09-10  
PRIOR APPLICATION NUMBER: GB 0220913.8  
PRIOR FILING DATE: 2002-09-10  
PRIOR APPLICATION NUMBER: PCT/GB02/05137  
PRIOR FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: PCT/GB02/05133  
NUMBER OF SEQ ID NOS: 69  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 67  
LENGTH: 2556  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (891)  
OTHER INFORMATION: Variable amino acid  
US-11-050-346-67

Query Match  
Best Local Similarity 45.0%; Score 40.5; DB 7; Length 2556;  
Best Local Similarity 61.5%; Pred. No. 1.8e+02;  
Matches 8; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Oy 5 ICTCQI-KTGPAC 16  
Db 397 ICTCPSGYTGAPAC 409

RESULT 28  
US-10-793-626-2510  
Sequence 2510, Application US/10793626

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; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STRAPHILOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P0348005
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2510
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (205)
; OTHER INFORMATION: variable amino acid
US-10-793-626-2510
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Query Match          44.4%; Score 40; DB 6; Length 205;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY      4  GLCTCQIKTG 13
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Db      141  GLCTCDVSTG 150
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RESULT 29
US-10-894-592-3
; Sequence 3, Application US/10894592
; Publication No. US20060019335A1
; GENERAL INFORMATION:
; APPLICANT: Du, Chunying
; TITLE OF INVENTION: Compositions and Methods to Promote c-IAP Autodegradation
; FILE REFERENCE: 68175
; CURRENT APPLICATION NUMBER: US/10/894,592
; CURRENT FILING DATE: 2004-07-20
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-894-592-3
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Query Match          44.4%; Score 40; DB 6; Length 1356;
Best Local Similarity 53.8%; Pred. No. 12e+02;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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QY      4  GLCTCQIKTG 16
          |||  |||
Db      893  GCCTCTGTGTGTC 905
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RESULT 30
US-11-096-051-12
; Sequence 12, Application US/11096051
; Publication No. US20050244868A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Rameesh
; APPLICANT: MacLachlan, Timothy K
; APPLICANT: Rastelli, Luca
; APPLICANT: Verne, Corine
; APPLICANT: Ettenberg, Seth
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use
; FILE REFERENCE: Attorney Docket No. Cura 967
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; CURRENT APPLICATION NUMBER: US/11/096,051
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/038,854
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 10/455,772
; PRIOR FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 60/557,978
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 12
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-096-051-12
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Query Match          43.9%; Score 39.5; DB 7; Length 257;
Best Local Similarity 57.1%; Pred. No. 33;
Matches 8; Conservative 1; Mismatches 4; Indels 1; Gaps 1;
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QY      4  GLCTCQIK-TGPAC 16
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Db      177  GTCRCCEGWTGPAC 190
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Search completed: April 3, 2006, 08:07:30
Job time : 13 secs
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